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PATENT

Docket No. 3116-1192

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this New Application Transmittal and the documents referred to as enclosed therein are being deposited with the United States Postal Service on this 11 Monday of October 2000 in an envelope as "Express Mail Post Office to Addressee" Mailing Label Number EL530609111US addressed to: Box Patent Application, Assistant Commissioner of Patents, Washington, D.C. 20231.

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Box Patent Application
Assistant Commissioner of Patents
Washington, D.C. 20231

NEW APPLICATION TRANSMITTAL

Transmitted herewith for filing is the patent application of

Inventor(s): Curtiss, Roy, III

For : Functional Balanced-Lethal Host-Vector Systems

Enclosed are:

1. Benefit of Prior U.S. Application (35 USC)

 The new application being transmitted claims the benefit of a and enclosed is added page for new application transmittal where benefit of a prior U.S. application claimed.

2. The Papers Required For Filing Under 37 CFR 1.53:

<u>57</u>	Pages of Specification
<u>1</u>	Pages of Abstract
<u>6</u>	Pages of Claims
<u>18</u>	Sheets of Drawing
<u>6</u>	Sheets of Sequence Listing

 X formal informal

In addition to the above papers there is also attached:

<u> </u>	Pages of an Amendment
<u> X </u>	Return Receipt Postcard
<u> </u>	Information Disclosure Statement with <u> </u> copies of references.

3. Declaration or oath

 x Enclosed 3 pages
 x Newly executed (original or copy)
 Copy from a prior application (continuation/divisional with page 5 of 5 completed)
 Deletion of Inventor(s) (signed statement attached deleting inventor(s) of prior application)
 Not enclosed

4. Inventorship Statement

The inventorship for all the claims in this application are:

 x the same

OR

 are not the same and an explanation, including the ownership of the various claims at the time the last claimed invention was made, is submitted.

5. Language

 X English Non-English

A verified English translation of the

[check applicable item(s)]

 specification and claims

 declaration

is attached.

6. Assignment

 x An assignment of the invention to Washington University

 x is filed under separate cover sheet

 was filed in the prior application

 will follow

7. Certified Copy

(Country) (Application No.) (Filed)

from which priority is claimed

 is attached

 will follow

8. Fee Calculation

CLAIMS AS FILED

	Number Filed	Provided with Basic Fee	Number Extra	Rate	Basic Fee \$710
Total Claims	44	20	24	X \$18.00	\$ 432.00
Independent Claims	5	3	2	X \$80.00	\$ 160.00
Multiple Dependent Claim(s), if any	0	0	0	X \$270.00	\$.00

☐ Amendment canceling extra claims enclosed

☐ Amendment deleting multiple dependencies enclosed

☐ Fee for extra claims is not being paid at this time

Filing Fee Calculation

\$1,302.00

9. Small Entity Statement

☐ verified statement that this is a filing by a small entity under 37 CFR 1.9 and 1.27 is attached.

Filing Fee Calculation (50% of above)

\$ _____

10. Fee Payment Being Made At This Time

☒ Enclosed

☒ basic filing fee

\$ 1,302.00

Total fees enclosed

\$ 1,302.00

11. Method of Payment of Fees

☒ check in the amount of \$ 1,302.00

12. Authorization to Charge Additional Fees

 X The Commissioner is hereby authorized to charge the following additional fees which may be required to Account No. 18-1829;

 X 37 CFR 1.16 (filing fees and presentation of extra claims)

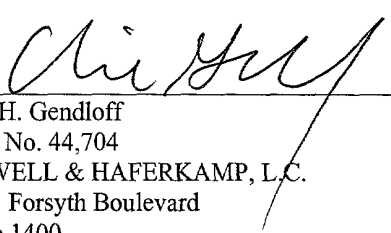
 X 37 CFR 1.17 (application processing fees)

 37 CFR 1.18 (issue fee at or before Mailing of Notice of Allowance, pursuant to 37 CFR 1.311(b)).

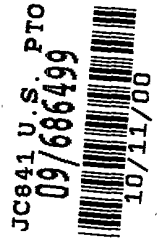
13. Instructions As To Overpayment

 X credit Account No. 18-1829

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PATENT

FUNCTIONAL BALANCED-LETHAL HOST-VECTOR SYSTEMS

Reference to Government Grant

This invention was made with government support under Grant Numbers DE06669 AI24533 and HD29099. The government has certain rights in this invention.

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Background of the Invention

(1) Field of the Invention

The invention relates to materials and methods for preparing vaccines, and more particularly to genetically engineered microorganisms which are useful to express desired gene products in the immunized animal host because they are balanced lethals which can be maintained as a genetically stable population within the immunized animal host.

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(2) Description of the Related Art

References Cited:

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U.S. Patent No. 4,190,495.

U.S. Patent No. 4,424,065.

U.S. Patent No. 4,550,081.

U.S. Patent No. 4,888,170.

U.S. Patent No. 5,006,335.

U.S. Patent No. 5,294,441.

U.S. Patent No. 5,278,744.

U.S. Patent No. 5,387,744.

U.S. Patent No. 5,389,368.

U.S. Patent No. 5,424,065.

U.S. Patent No. 5,468,485.

U.S. Patent No. 5,527,529.

U.S. Patent No. 5,643,771.

5 U.S. Patent No. 5,656,488.

U.S. Patent No. 5,672,345.

U.S. Patent No. 5,840,483.

U.S. Patent No. 5,851,519.

U.S. Patent No. 5,855,879.

10 U.S. Patent No. 5,855,880.

U.S. Patent No. 5,888,799.

U.S. Patent No. 5,980,907.

U.S. Patent No. 6,024,961.

15 Related Art:

Genetically engineered microorganisms have widespread utility and importance. One important use of genetically engineered microorganisms is as a live vaccine for inducing immunity. See, e.g., U.S. Patents 6,024,961; 4,888,170; 5,389,368; 5,855,879; 5,855,880; 5,294,441; 5,468,485; 5,387,744; 5,840,483, 5,672,345; 5,424,065; 5,888,799; 5,424,065; 20 5,656,488; 5,006,335; 5,643,771; 5,980,907; 5,851,519; and 5,527,529, all of which are incorporated by reference. When the genetically engineered microorganism is to be utilized as a vertebrate live vaccine, certain considerations must be taken into account. To provide a benefit beyond that of a nonliving vaccine, the live vaccine microorganism must attach to, invade, and survive in lymphoid tissues of the vertebrate and expose these immune effector 25 sites in the vertebrate to antigen for an extended period of time. By this continual stimulation, the vertebrate's immune system becomes more highly reactive to the antigen than with a nonliving vaccine. Therefore, preferred live vaccines are attenuated pathogens of the vertebrate, particularly pathogens that colonize the gut-associated lymphoid tissue (GALT) or bronchial-associated lymphoid tissue (BALT). An additional advantage of these attenuated 30 pathogens over nonliving vaccines is that these pathogens have elaborate mechanisms to gain access to lymphoid tissues, and thus efficient exposure to the vertebrate's immune system can be expected. In contrast, nonliving vaccines will only provide an immune stimulus if the vaccine is passively exposed to the immune system, or if host mechanisms bring the vaccine to the immune system.

Despite their advantages over non-living vaccines, effective live vaccines must overcome certain obstacles. Genetically engineered microorganisms used as vaccines for antigen delivery must synthesize a gene product from which it derives no benefit, and the high level expression of the recombinant protein may be deleterious to the microorganism. Thus, the genetically engineered microorganism may be at a selective disadvantage relative to the same type of microorganism that does not produce the cloned gene product. As a result, when the vaccine is being manufactured, e.g., in a fermentor during production of the vaccine, spontaneous segregants that have lost the DNA sequence specifying the desired gene product quickly outpopulate the genetically engineered microorganism. This loss of the antigen-producing DNA sequence can also occur to the vaccine after inoculation into the host animal. Therefore, selection mechanisms have been developed which are designed to maintain the antigen-producing DNA sequence in the microorganism population.

One method for applying selective pressure to a bacterial population to maintain production of the desired polypeptide is to insert the recombinant gene encoding the polypeptide in a plasmid that also contains a gene encoding antibiotic resistance. Most cloning vectors currently in use have one or more genes specifying resistance to antibiotics. Thus, antibiotics can be added to the culture medium for growth of genetically engineered microorganisms to kill those bacteria that have lost the recombinant plasmid. This practice has several drawbacks. First, it is expensive to add antibiotics to growth medium. Second, since antibiotic resistance is often based upon the synthesis of drug inactivating enzymes, cells remain phenotypically drug resistant for a number of cell generations after the loss of genes for drug resistance and the linked desired gene. Third, in the case of genetically engineered bacteria to be used as a live vaccine, the United States Department of Agriculture and the Food and Drug Administration have refrained from approving strains which express antibiotic resistance.

An alternative to the use of antibiotic resistance for maintaining a recombinant plasmid and/or a cloned gene in a genetically-engineered microorganism is the use of a mutant microorganism that lacks a critical biosynthetic enzyme, and supplying the wild-type gene for that enzyme on the plasmid cloning vector. See, e.g., Kahn et al (1979) and Dean (1981). Unfortunately, this is impractical in many situations. The use of mutants which are missing enzymes involved in the biosynthesis of amino acids, purines, pyrimidines, and vitamins often does not preclude the growth of these mutants since the end-product of the pathway which is required for growth is often furnished by the environment. For example, inexpensive media used for the growth of recombinant organisms in fermenters often contain

these end products. In addition, particularly in the case of live vaccines, the end product may be supplied *in vivo* by the vaccinated host.

The problems of genetic instability of genetically engineered microorganisms possessing a cloned gene on a plasmid can arguably be alleviated by integrating the cloned gene into the chromosome of the microorganism. However, integration of the recombinant gene into the chromosome overcomes many of the potential benefits of having it reside on the plasmid. For example, control of plasmid copy number by, for example, selection of the plasmid containing the cloned gene provides a mechanism for increasing the product yield. It is to be noted that the level of expression of a gene is usually proportional to gene copy number, which increases with increasing plasmid copy number. The use of plasmids with a regulatable promoter also offer one mechanism for temporally controlling the expression of the product so that high level expression occurs at less deleterious times during the growth cycle.

All bacteria have a peptidoglycan layer of the cell wall that imparts shape and rigidity. The peptidoglycan is made of a polymer of repeating muramic acid-N-acetylglucosamine units and is cross-linked by short peptides. In all Gram-negative bacteria and in *Mycobacterium* and in *Nocardia* species of Eubacteria, the peptide is composed of L-alanine, D-glutamic acid, mesodiaminopimelic acid (DAP), and D-alanine. In most Gram-positive microorganisms the DAP component is replaced by its decarboxylation product L-lysine.

As illustrated by Figure 1, DAP is synthesized in six enzymatic steps from β -aspartic semialdehyde, which, in turn, is synthesized in two steps from L-aspartic acid. In the first step, L-aspartic acid is phosphorylated by one of several (usually three) β -aspartokinases which are encoded by several (usually three) separate genes regulated independently by repression and/or feedback inhibition of the gene products by the ultimate end products L-threonine, L-methionine, and L-lysine. β -aspartyl phosphate is converted in one step to β -aspartic semialdehyde by β -aspartate semialdehyde dehydrogenase, the product of the *asd* gene. Mutants with a point mutation in or deletion of the *asd* gene as well as mutants with mutations in any of the six genes specifying the enzymes for converting β -aspartate semialdehyde to DAP require DAP in all media. When DAP-requiring mutants are deprived of DAP they undergo DAP-less death and lysis, releasing their contents.

The inclusion of *asd*, and thus *dap*, mutations in strains of bacteria affords biological containment, since such mutant strains are unable to survive in environments other than a carefully controlled laboratory environment. The basis for this has been extensively described in U.S. Patent 4,190,495.

The gene for β -aspartate semialdehyde dehydrogenase from *Streptococcus mutans* PS14 (UAB62) has been cloned and expressed in *asd* mutants of *E. coli* (Jagusztyn-Krynicka, et al, 1982; Curtiss et al, 1982). Subsequently, the *S. mutans asd* gene was sequenced (Cardineau and Curtiss, 1987). The gene for β -aspartate semialdehyde dehydrogenase from *Salmonella typhimurium* has also been cloned and expressed in *asd* mutants of *E. coli* (Galán et al., 1990). Subsequently, the *S. typhimurium asd* gene was sequenced (SEQ ID NO:1) and its amino acid sequence determined (SEQ ID NO:2). Both sequences are found in Genbank accession number AF 015781.

U.S. Patent No. 5,672,345 discloses a method of maintaining a desired recombinant gene in a genetic population of bacterial cells expressing the product of the desired recombinant gene. The method utilizes host cells having a mutation in a chromosomal gene encoding an enzyme that catalyzes a step in the biosynthesis of an essential cell wall component such as DAP. The host cells are transformed with two recombinant genes in physical linkage: one gene encoding a polypeptide that functionally replaces the enzyme and the other gene encoding the desired gene product. Loss of the recombinant gene complementing the mutant host gene causes the bacterial cells to lyse when in an environment requiring expression of the enzyme. The specification of patent 5,672,345 teaches that it is preferable that the non-functional chromosomal gene lack homology with its complementing plasmid gene, or have an extensive enough mutation (e.g., by utilizing a deletion mutation which eliminates the entire gene and/or flanking sequences) to preclude the ability of the complementing plasmid gene from recombining to replace the defective chromosomal gene by two crossover events on either side of the defective chromosomal gene. Such a lack of recombination maximizes the stability of the gene encoding the desired gene product by maintaining the linked selective pressure with the complementing recombinant plasmid gene.

However, avoiding homology between both sides of the inactivating chromosomal gene mutation and its functional plasmid counterpart precludes the use of many useful combinations of these genes. Therefore, it would be desirable to be able to utilize mutant chromosomal genes with complementing plasmid genes having such homology.

Summary of the Invention

Briefly, therefore, the inventor has succeeded in discovering that balanced-lethal host-vector systems, similar to those described in U. S. Patent No. 5,672,345, may usefully comprise an extrachromosomal vector that has homology with both sides of the chromosomal mutation that inactivates the native gene which is complemented in the vector. Such homology allows a double crossover to occur between these homologous regions, permitting

replacement of the defective chromosomal gene with the active recombinant copy on the vector. In most useful situations, the homology resides between regions flanking the inactivating mutation and its complementing plasmid gene. These flanking regions would often be outside of the inactivated chromosomal gene, particularly if the chromosomal gene is inactivated by a deletion. Preferably, the plasmid also comprises a desired gene, providing linkage between the complementing plasmid gene and the desired gene. The desired gene encodes a desired polypeptide, for example an antigen. This invention provides for the utilization of complementing genes that have this mutation-flanking homology to its inactivated chromosomal counterpart.

Also discovered and disclosed herein is means to reduce the level of expression of the complementing recombinant gene on the vector to the lowest level needed for complementation and to preclude lysis of the bacteria when the complementing plasmid recombinant gene is expressed. This is accomplished through the selective use of particular origins of replication that set particular plasmid copy numbers in conjunction with changes in the regulatory DNA sequences 5' to the complementing recombinant gene. In one aspect of these embodiments, the -35 recognition sequence and promoter -10 sequence of the complementing recombinant gene is absent. When such vectors have a high copy number origin of replication and are transfected into a microorganism lacking a functional *asd* gene, enough *asd* is made from the vector to allow synthesis of sufficient DAP to maintain viability of the microorganism. The above means for reducing the level of the essential gene can be utilized in any of the embodiments described below.

The present invention also teaches the means to generate defined deletions of the native essential gene and to insert therein a gene encoding a protein that can be detected to verify the presence of the mutant chromosomal gene.

Accordingly, the present invention is directed to a microorganism with a cell wall comprising diaminopimelic acid (DAP). The microorganism further comprises (a) an inactivating mutation in a native chromosomal essential gene encoding an essential enzyme which catalyzes a step in the biosynthesis of DAP; (b) a recombinant complementing gene encoding a functional replacement for the essential enzyme, where the complementing gene is on an extrachromosomal vector that is capable of homologous recombination with the chromosome; and (c) a desired gene on the extrachromosomal vector, where the desired gene is a recombinant gene encoding a desired gene product. In progeny populations of the microorganism, the desired gene is stably maintained. Preferably, the microorganism is a bacterium and the extrachromosomal vector is a plasmid. In many embodiments, the bacterium is a member of the *Enterobacteriaceae*. The bacterium is often an attenuated

derivative of a pathogenic *Salmonella* that attaches to, invades and persists in the gut-associated lymphoid tissue or bronchial-associated lymphoid tissue. The bacterium is often attenuated through the use of inactivating mutations in native genes. Preferred attenuating mutations are in the following genes: a *pab* gene, a *pur* gene, an *aro* gene, *asd*, a *dap* gene, *nadA*, *pncB*, *galE*, *pmi*, *fur*, *rpsL*, *ompR*, *htrA*, *hema*, *cdt*, *cya*, *crp*, *dam*, *phoP*, *phoQ*, *rfc*, *poxA*, *galU*, *mviA*, *sodC*, *recA*, *ssrA*, *sirA*, *inv*, *hilA*, *rpoE*, *flgM*, *tonB*, *slyA*, and combinations thereof. The most preferred attenuating mutations are *aroA*, *aroC*, *aroD*, *cdt*, *cya*, *crp*, *phoP*, *phoQ*, *ompR*, *galE*, and *htrA*.

The microorganisms of the present invention may be utilized to induce an immune response in a vertebrate that has been inoculated with them. In these embodiments, the microorganism is preferably a member of the *Enterobacteriaceae*, most preferably, the attenuated *Salmonella* described above. The most preferred *Salmonella* species are *S. typhimurium*, *S. typhi*, *S. paratyphi*, *S. choleraesuis*, *S. dublin* and *S. gallinarum*. As is known, each of these *Salmonella* species may have preferred host species, where wild-type strains are pathogenic. See, e.g., U.S. Patents 5,468,485 and 4,550,081. Also, the desired gene product in these embodiments is preferably an antigen. Preferred antigens are bacterial antigens, viral antigens, fungal antigens, parasitic antigens, gamete-specific antigens, allergens, and tumor antigens.

Preferred genes that encode the essential enzymes of the above-described bacteria are *dapA*, *dapB*, *dapD*, *dapE*, and *dapF*. The most preferred essential gene is a β -aspartic semialdehyde dehydrogenase gene, denoted *asd*. Preferred inactivating mutations in these genes are deletions and insertions, for example transposon insertions and insertions with a gene encoding a phenotypically detectable reporter gene. Preferred inactivating mutations are mutations that do not normally revert to wild type, such as *Tn10* insertions, insertions of a *xylE* gene, and deletion mutations such as $\Delta asdA16$, $\Delta asdA1$, $\Delta asdA13$ and $\Delta asdA4$.

The desired gene can also be operably linked to a eukaryotic promoter, preferably a CMV promoter, to create a eukaryotic expression vector that serves as a DNA vaccine where the desired gene is transcribed and translated directly by the vertebrate. The DNA vaccine can be introduced into the vertebrate directly or it can be delivered to the vertebrate by live microorganisms such as the *Enterobacteriaceae* described herein.

The present invention is also directed to the recombinant vectors, preferably plasmids, which are useful in the above microorganisms. As indicated previously, the preferred recombinant complementing gene in those plasmids are *asd* genes. In more preferred embodiments the *asd* is from a member of the *Enterobacteriaceae*, such as *Salmonella typhimurium*. When the desired gene on the plasmid encodes an antigen,

preferred antigens are colonization antigens, i.e. virulence antigens, generally on the surface of pathogens, that promote the ability of a pathogen to infect an animal or human host.

Examples include adhesins and invasins (Salyers and Whitt, 1994). Other preferred desired genes encode products that affect vertebrate immunity, such as lymphokines, cytokines, and sperm-specific or egg-specific autoantigens.

Additionally, the present invention is directed to methods of selecting for the presence of a desired gene in a population of microbial cells. The methods comprise (a) transfecting a microbial cell with a plasmid as described above, the microbial cell having an inactivating mutation in a native chromosomal gene encoding the essential enzyme, as previously discussed; and (b) culturing the microbial cell.

Preferred embodiments of these methods utilize microbial cells that are members of the *Enterobacteriaceae* and essential genes that are *dap* or *asd* genes. Additionally, the microbial cells may usefully be attenuated derivatives of pathogenic *Salmonella* that attach to, invade and persist in the gut-associated lymphoid tissue or bronchial-associated lymphoid tissue. As previously discussed, when these attenuated strains are the above attenuated *Salmonella*, preferred attenuating mutations are in the following genes: a *pab* gene, a *pur* gene, an *aro* gene, *asd*, a *dap* gene, *nadA*, *pncB*, *galE*, *pmi*, *fur*, *rpsL*, *ompR*, *htrA*, *hemA*, *cdt*, *cya*, *crp*, *dam*, *phoP*, *phoQ*, *rfc*, *poxA*, *galU*, *mviA*, *sodC*, *recA*, *ssrA*, *sirA*, *inv*, *hilA*, *rpoE*, *flgM*, *tonB*, *slyA*, and combinations thereof.

The microbes useful for these methods also may have any of the characteristics previously discussed. The culturing of these microbes may be in a vertebrate or *in vitro*.

Additionally, the present invention is directed to a vaccine for immunization of a vertebrate. The vaccine comprises live bacterial cells of an attenuated derivative of a pathogenic bacterium in a pharmaceutical carrier. The bacterial cells are as previously described, with any of the appropriate features and limitations discussed above. Preferably, the extrachromosomal vector is a plasmid, the bacterium is a *Salmonella*, and the essential gene is an *asd* gene. The complementing gene may be from the same *Salmonella* species as the bacterial cell. For these embodiments, the desired gene product is an antigen, as previously described. An additional embodiment of the invention is thus a method of

inducing immunoprotection in a vertebrate, where the method comprises administering to the vertebrate the vaccine described above. The vaccines of these embodiments can be utilized as DNA vaccines when the desired gene is operably linked to a eukaryotic promoter, for example a CMV promoter. As previously discussed, these DNA vaccines can be delivered by bacteria or by direct introduction of the DNA into the vertebrate.

In additional embodiments, the present invention is directed to a method of delivering a desired gene product to a vertebrate. The method comprises administering to the vertebrate live bacterial cells of an attenuated derivative of a pathogenic bacterium. The bacterial cells are as described above. In these embodiments the preferred bacteria are *Salmonella*, most preferably *S. typhimurium*, *S. typhi*, *S. paratyphi*, *S. choleraesuis*, *S. dublin* or *S. gallinarum*. As before, preferred attenuating mutations are in a *pab* gene, a *pur* gene, an *aro* gene, *asd*, a *dap* gene, *nadA*, *pncB*, *galE*, *pmi*, *fur*, *rpsL*, *ompR*, *htrA*, *hemA*, *cdt*, *cya*, *crp*, *dam*, *phoP*, *phoQ*, *rfc*, *poxA*, *galU*, *mviA*, *sodC*, *recA*, *ssrA*, *sirA*, *inv*, *hlyA*, *rpoE*, *flgM*, *tonB*, *slyA*, and combinations thereof, and the most preferred essential gene is an *asd*. Preferred desired gene products in these embodiments include antigens, lymphokines, cytokines, and sperm-specific or egg-specific autoantigens.

Other embodiments of the invention include the various novel plasmids and bacterial strains first described herein.

15 Brief Description of the Drawings

Figure 1 is a flow chart for the biosynthesis of the aspartic acid family of amino acids.

Figures 2A and 2B illustrate the nucleotide (SEQ ID NO:1) and encoded amino acid sequence (SEQ ID NO:2), respectively, of the *Salmonella typhimurium asdA* gene showing from 5' to 3': an upstream nucleotide sequence of 244 base pairs (bp); an open reading frame (ORF) of 1176 bp containing two *EcoRV* sites (indicated by underlining) separated by 729 bp; and a downstream sequence of 315 bp; with the start and stop sites indicated by bold letters.

Figure 3 illustrates the structure of pMEG-006, a *pir*-dependent suicide vector with the $\Delta asdA16$ mutation.

Figure 4 illustrates the structure of pMEG-443, a *pir*-dependent suicide vector for allele replacement of the $\Delta asdA16$.

Figure 5 illustrates the composition of pMEG-223, a *pir*-dependent suicide vector containing the $\Delta asdA20::xylE$ construction for transfer of that mutation to the chromosome of *Salmonella* strains.

Figure 6A is a genetic map of the $\Delta asdA20::xylE$ defined deletion/insertion, showing common restriction sites and the *xylE* open reading frame. Figure 6B shows the nucleotide (SEQ ID NO:3) and encoded amino acid sequences (SEQ ID NO:4) of this genetic construct, showing from 5' to 3': the 244 bp *asd* upstream sequence, an ORF containing the first 273 bases of the 5' portion of the *asdA* ORF encoding SEQ ID NO:5 (marked as "a" along the bottom of the sequence), a 955 bp fragment of the *xylE* gene, which encodes SEQ ID NO:6

and which replaces a deletion of the *asdA* gene between the *EcoRV* sites (marked as "c"), a 174 bp region from the 3' portion of the *asdA* ORF (marked as "b"); and the 315 base pair *asdA* downstream sequence (SEQ ID NO:7). Various restriction sites are also shown in Figure 6B.

5 Figure 7 depicts the *trc* promoter and the multiple cloning site present in pYA3332, pYA3333, pYA3334, pYA3341 and pYA3342 (SEQ ID NO:8).

10 Figure 8 illustrates the composition of Asd⁺ cloning vectors with low, moderate and high plasmid copy numbers due to the p15A, pBR and pUC replicons, respectively, represented by pYA3332, pYA3333, and pYA3334, respectively, all of which have been engineered to possess a multiple cloning site with the *NcoI* restriction site to enable cloning of full-length coding sequences starting with an ATG codon.

Figure 9 depicts the moderate (pBR) and high (pUC) copy number Asd⁺ plasmid vectors pYA3342 and pYA3341 that have been engineered to reduce the level of Asd protein expressed due to deletion of the *asd* gene -35 and -10 promoter sequences.

15 Figure 10 depicts a SDS polyacrylamide gel of extracts of *S. typhimurium* strains after staining with Coomassie Brilliant Blue to reveal the level of Asd protein specified by the Asd⁺ plasmids pYA3333, pYA3334, pYA3342 and pYA3341.

20 Figure 11 represents an illustration of the extent of sequences encoding the wild-type *asd* gene and its 5' and 3' flanking sequences as found on various Asd⁺ vectors and the extent of deletions with or without the *xylE* insertion in the chromosome of constructed *S. typhimurium* strains to depict in a scale model the possible regions in which recombination between homologous sequences on the vector and the chromosome might occur.

25 Figure 12 depicts the composition of a high-copy number Asd⁺ vector with the SD-*asd* sequence and designed with eukaryotic expression elements to be used for construction of DNA vaccine vectors that could be harbored and produced in bacterial strains with a Δ *asd* mutation or delivered directly to the immunized host by attenuated bacterial strains also possessing a Δ *asd* mutation.

Detailed Description of the Invention

30 **A. Definitions**

"Recombinant host cells", "host cells", "cells" and other such terms denoting microorganisms are used interchangeably, and refer to cells which can be, or have been, used as recipients for recombinant vectors or other transferred DNA, and include the progeny of the original cell transfected. It is understood that the progeny of a single parental cell may not

necessarily be completely identical in genomic or total DNA complement as the original parent, due to accidental or deliberate mutation.

A "progeny population" means the population of living bacterial cells in a culture propagated from a single, recombinant bacterial cell. Unless otherwise defined, a recombinant gene on an extrachromosomal vector is "stably maintained" in a progeny population when the majority of the cells in a population lacking a native essential gene complemented by the recombinant gene are both able to survive in a particular environment (e.g., lacking diaminopimelic acid (DAP)) and retain and/or express a desired gene that is linked to the recombinant gene. Preferably, at least 90% of the cells in the population survive and retain the desired gene; more preferably, at least 99% of the cells survive.

"Control sequence" refers to a DNA sequence that is necessary to effect the expression of a coding sequence to which it is operably linked. As such, control sequences provide sites for the action of repressors, activators, enhancers, RNA polymerase, and other transcription factors. Nonlimiting examples of control sequences are promoters, ribosome binding sites, transcription terminator sequences, and translation stop sequences.

Control sequences permitting expression of gene products in bacteria are distinctly different from control sequences necessary for gene expression in eukaryotic organisms such that prokaryotic control sequences generally do not function in eukaryotic cells and vice versa. The term "control sequence" can encompass those sequences from prokaryotes or eukaryotes.

"Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is present in the cell in such a way that expression of the coding sequence may be influenced by the action of the control sequence.

"Gram-negative bacteria" include cocci, nonenteric rods, enteric rods and spirilla. Non-limiting examples of genera of Gram-negative bacteria include *Neisseria*, *Spirillum*, *Pasteurella*, *Brucella*, *Yersinia*, *Francisella*, *Haemophilus*, *Bordetella*, *Escherichia*, *Salmonella*, *Shigella*, *Klebsiella*, *Bartonella*, *Ehrlichia*, *Legionella*, *Enterobacteria*, *Proteus*, *Vibrio*, *Pseudomonas*, *Xanthomonas*, *Myxococcus*, *Erwinia*, *Bacteroides*, *Acetobacter*, *Aerobacter*, *Agrobacterium*, *Azotobacter*, *Spirilla*, *Serratia*, *Vibrio*, *Rhizobium*, *Chlamydia*, *Rickettsia*, *Trepanema*, *Fusobacterium*, *Borrelia* and *Trepanema*.

"Gram-positive bacteria" include cocci, nonsporulating rods, and sporulating rods. Non-limiting examples of genera of Gram-positive bacteria include *Actinomyces*, *Bacillus*, *Clostridium*, *Corynebacterium*, *Erysipelothrix*, *Lactobacillus*, *Listeria*, *Mycobacterium*, *Nocardia*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*.

A "mutation" is an alteration of a polynucleotide sequence, characterized either by an alteration in one or more nucleotide bases, or by an insertion of one or more nucleotides into the sequence, or by a deletion of one or more nucleotides from the sequence, or a combination of these.

5 A "gene" is a biological unit of heredity. Generally, a gene is a polynucleotide sequence that encodes an RNA molecule or a polypeptide, or a mutation of said polynucleotide sequence. The gene may be a naturally occurring sequence that is capable of being expressed into an active or inactive polypeptide. The gene may also comprise a mutation, for example a point mutation, insertion, or deletion, such that it is not capable of
10 being expressed, or such that it expresses an altered or truncated polypeptide or RNA molecule. A gene may be created by recombinant DNA methodologies. Alternatively, the gene may be synthesized by well-known synthetic methods.

A "native gene" is a gene as it occurs in a wild-type organism, for example, the gene encoding β -aspartic semialdehyde dehydrogenase (Asd) in *E. coli* or *Salmonella*, the genes
15 encoding alanine racemase, and the genes encoding D-alanyl-D-alanine ligase. Other examples of native genes are described infra.

A "recombinant gene," as used herein, is defined as an identifiable polynucleotide sequence within a larger polynucleotide sequence that is not found in that form and position in the larger sequence in nature. The recombinant gene can be, for example, a wild-type gene
20 that is inserted in a non-native position in the chromosome, or a mutant form of the wild-type gene in the native position. As used herein, recombinant genes are the product of genetic engineering manipulations performed in vitro.

As used herein, "recombination" or "genetic recombination" is the joining or exchange of portions of two DNA molecules within a living cell. In homologous
25 recombination, the joining or exchange occurs where the two DNA molecules are homologous. The exchange can occur by way of a single crossover (i.e., point of exchange) between the two molecules. Alternatively, the exchange can occur between two separate homologous regions of either or both of the molecules (double crossover). Non-homologous recombination may be mediated by genetic elements such as transposons.

30 An "essential gene" is a gene that encodes a function that is required for cell viability. Essential genes may be functional, that is they are providing the essential function. Essential genes may also be non-functional, for example by having mutations that render the translated protein non-functional, or by not being operably linked to a control element essential for transcription of the gene. There also may be more than one functional copy of an essential

gene in a microbial cell, for example one gene on a plasmid and the other on the chromosome. As such, the loss of any one copy of the essential gene would not be fatal to the cell.

Unless otherwise indicated, essential genes of the present invention encode an enzyme that catalyzes a step in the biosynthesis of diaminopimelic acid (DAP), an essential cell wall component in many microbes. An example of an essential gene is *asd*, encoding β -aspartic semialdehyde dehydrogenase. Microbes which are deficient in *asd* gene function will grow on media containing DAP, L-methionine and L-threonine, or DAP and homoserine.

An "essential cell wall component" is one that is necessary to maintain the structural integrity of the cell wall. Examples of essential cell wall components of prokaryotes include glycans, particularly peptidoglycans. While the use of genes encoding enzymes for bacterial cell wall synthesis are exemplified herein, the skilled artisan would recognize that the methods provided herein can be utilized with other prokaryotic cell wall containing organisms.

A "peptidoglycan" is a typical constituent of cell walls of almost all prokaryotic cells. These molecules are responsible for the rigidity of the cell wall. Peptidoglycans are a family of macromolecules containing acylated amino sugars and three to six different amino acids; the heteropolymers contain glycan strands crosslinked through short peptides. Peptidoglycans have been reviewed in Schleifer and Kandler (1972).

As used herein, "DAP" refers to both stereoisomers of diaminopimelic acid and its salts, i.e., both the LL- and meso- forms, unless otherwise shown by specific notation.

The gene symbols for mutant strains utilized herein are those described by O'Brian (1993), and Sanderson et al., Chapter 110 in Neidhardt et al., 1996. The symbols used for transposons, particularly Tn10, follow the convention used in Altman et al., Chapter 141 in Neidhardt et al., 1996.

An "individual" treated with a vaccine of the invention is defined herein as including all vertebrates, for example, mammals, including domestic animals and humans, various species of birds, including domestic birds, particularly those of agricultural importance. In addition, mollusks and certain other invertebrates have a primitive immune system, and are included as an "individual".

"Transfection" or "transformation," as used herein, refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, direct uptake (naturally or by electroporation), transduction, or conjugation. The exogenous polynucleotide may be maintained as a plasmid, or alternatively, may be integrated into the host chromosome.

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physiological function. Attenuated strains are incapable of inducing a full suite of symptoms of the disease that is normally associated with its pathogenic counterpart. Sometimes "avirulent" is used as a substitute term for attenuated.

As used herein, "microbe" or "microorganism" includes bacteria, protozoa, and unicellular fungi.

As used herein, "DNA vaccine" refers to a DNA molecule, preferably a plasmid, that has a gene sequence encoding a desired gene product operably linked to a eukaryotic control sequence, so that the desired gene product is expressed maximally after introduction of the DNA vaccine internally into eukaryotic cells by vaccination (immunization). The DNA vaccine can be administered to individuals to be immunized by injection, air gun or preferably by use of attenuated bacteria that liberate the DNA vaccine on entrance into host cells of the immunized individual. *See, e.g.,* Detrich et al. (1999); Detrich and Globel (2000); Herrmann et al., (1999); Krieg et al. (1998); Ulmer et al. (1996a); Ulmer et al. (1996b).

B. General Description

Unless otherwise indicated, the practice of the present invention employs conventional techniques of cell culture, molecular biology, microbiology, recombinant DNA manipulation, immunology and animal science, which are within the skill of the art. Such techniques are explained fully in the literature. *See, e.g.,* DNA CLONING, Volumes I and II (D.N. Glover, ed., 1985); OLIGONUCLEOTIDE SYNTHESIS (M.J. Gait ed., 1984); NUCLEIC ACID HYBRIDIZATION (B.D. Hames and S.J. Higgins, eds., 1984); B. Perbal, A PRACTICAL GUIDE TO MOLECULAR CLONING (1984); the series, METHODS IN ENZYMOLOGY (Academic Press, Inc.); VECTORS: A SURVEY OF MOLECULAR CLONING VECTORS AND THEIR USES (R.L. Rodriguez and D.T. Denhardt, eds., 1987, Butterworths); Sambrook et al. (1989), MOLECULAR CLONING, A LABORATORY MANUAL, second ed., Cold Spring Harbor Laboratory Press; and Ausubel et al. (1995), SHORT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley and Sons.

This invention is directed to genetically engineered microbial host cells that stably maintain a desired recombinant gene in progeny populations. The host cells in this population have an inactivating mutation in a native essential gene encoding an enzyme that is essential for cell survival in that the enzyme catalyzes a step in the biosynthesis of an essential cell wall component. In addition, a recombinant complementing essential gene, genetically linked to a desired gene product, replaces the function of the inactivated essential gene. The invention describes methods for creating and isolating cells that are suitable host cells. Also disclosed

are extrachromosomal vectors, particularly plasmids, which are suitable for transfecting microbial host cells. These plasmids comprise the recombinant complementing gene and the gene encoding the desired gene product. The cells of the invention are particularly suitable as components of vaccines, particularly live vaccines.

The cells of the invention are also suitable for the production of DNA vaccines which themselves can be used after isolation from the cells for direct immunization of individuals by recently developed DNA vaccine technologies (Ulmer et al., 1996a; Ulmer et al., 1996b; Whalen, 1996; Robinson, 1997). In these embodiments, the DNA vaccines are preferably produced as high copy number plasmid vectors in *E. coli*, where they can be easily purified by well known methods. It is also possible to use attenuated derivatives of bacterial pathogens to deliver DNA vaccine vectors to cells within the immunized individual (Sizemore et al., 1995; Hone et al., 1996; Pascual et al., 1997; Darji et al., 1997).

One characteristic of the host cells of the invention is that their cell walls contain a peptidoglycan comprised of diaminopimelic acid (DAP), which is necessary to maintain the structural integrity of the cell, i.e., without which the cell lyses, a victim of DAPless death. Examples of host cells in which the peptidoglycan is comprised of DAP are known to those of skill in the art, for example, see Schleifer and Kandler (1972), and include, for example probably all Gram-negative bacteria, as well as other organisms, such as Gram-positive bacteria in the genera *Mycobacterium* and *Nocardia*. A review of the methods by which a peptidoglycan may be characterized as containing DAP is presented in Schleifer and Kandler (1972).

Another characteristic of the host cells of the present invention is that they have been mutated so that a native chromosomal essential gene encoding an enzyme which catalyzes a step in the biosynthesis of DAP is not functional, i.e., does not yield a functional enzyme.

25 Methods for mutating cells to create the host cells of the invention are known in the art, and include, for example, chemical mutagenesis, UV mutagenesis, mutations induced via the action of transposons, or defined deletion mutations using recombinant techniques. See, e.g., Curtiss, U.S. Patent 5,672,345; Miller (1992); Gebhardt et al. (1994); Miller and Mekalanos (1988) and Methods in Enzymology. Although host cells carrying point mutations in the

30 above-described genes are included in the invention, it is preferable to use host cells carrying deletion mutations in these genes, since deletion mutants do not generally revert.

Enzymes which catalyze the biosynthesis of DAP are known in the art. Figure 1 shows the pathway for the biosynthesis of the aspartate family of amino acids, of which both stereoisomers of DAP are members. For a review of the biosynthesis of this family of amino acids, see Umbarger, chapter 27 in Neidhardt et al.(1996). Examples of genes encoding

enzymes which catalyze steps in the biosynthesis of DAP are known in the art for a variety of organisms, see, for example, GENETIC MAPS 1987 (S.J. O'Brien, ed., Cold Spring Harbor Laboratories), and include, for example, the *dapA*, *dapB*, *dapC*, *dapD*, and *dapE* and *dapF* genes in *S. typhimurium* and in *E. coli*. Another enzyme which is essential for DAP synthesis is β -aspartic semialdehyde dehydrogenase (Asd), which is encoded by the *asd* gene.

Described in the Examples, infra, are methods for introducing deletion mutations in the above genes, particularly the *asd* gene (Δasd), in a diversity of bacterial strains, particularly members of the *Enterobacteriaceae*. Also described are methods to isolate *asd* mutants of other Gram-negative bacteria and mycobacteria. Table 1 lists the *E. coli* K-12 and *S. typhimurium* strains used to isolate *asd* mutants and their derivatives; the Asd⁻ strains listed therein are examples of strains which can be used to construct other strains, utilizing transposon techniques and also molecular genetic techniques for allele replacement, as described infra. Asd⁻ strains are also described in U.S. Patent Nos. 4,190,495, 5,672,345 and 5,840,483.

Table 1

Strain number	Parent strain/ plasmid	Relevant genotype	Bacterial strains	Derivation
<u>A. Escherichia coli strains</u>				
χ2108	K-12/F ⁻	<i>leu-50 tsx-98 proB59</i> Δ69[<i>lacZOP1</i>] Δ40[<i>gal-uvrB</i>] <i>rposL206 asdA4 argH70</i>		HNO ₂ -induced Asd ⁻ mutant of χ2087
χ2637	K-12/F ⁻	<i>tsx-63 purB41 glnV42 λ pyrF30</i> <i>his-53 tte-1 ΔasdA4 xyl-14</i> <i>cycB2 cycA1</i>		P1cml(χ2108) → χ660 with sel'n for AroB ⁺ <i>Asd</i> ⁻
χ2978	K-12/F ⁻	<i>tsx-63 purE41 glnv42 λ pyrF30</i> <i>his-53 tte-1 zhf-2::Tn10</i> <i>xyl-14 cycB2 cycA1</i>		P1L4(χ2842::Tn10 library) χ2637 with sel'n for Tc ^r Asd ⁺
χ2979	K-12/F ⁻	<i>tsx-63 purE41 glnv42 λ pyrF30</i> <i>his-53 tte-1 ΔasdA4 zhf-2::Tn10</i> <i>xyl-14 cycB2 cycA1</i>		P1L4(χ2978) → χ2637 with sel'n for Tc ^r
χ2981	K-12/F ⁻	Δ41[<i>proB-lacYZ</i>] <i>glnV42 λ tte-1</i> Δ <i>asdA4 zhf-2::Tn10 cycA1</i>		P1L4(χ2979) → χ354 with sel'n for Tc ^r Asd ⁻
χ2984	K-12/F ⁻	Δ41[<i>proB-lacYZ</i>] <i>λ tte-1 ΔasdA4</i> Δ[<i>zhf-2::Tn10</i>] <i>cycA1</i>		FA ^r Tc ^s derivative of χ2981
JM83	K-12/F ⁻	<i>ara</i> Δ[<i>lac-pro</i>] <i>λ rpsL thi ø80dlacZ</i> Δ <i>M15</i>		Viera and Messing
χ6096	K-12/F ⁻	<i>ara</i> Δ[<i>lac-pro</i>] <i>rpsL ΔasdA4</i> <i>zhf-2::Tn10 thi ø80dlacZ</i> Δ <i>M15</i>		P1L4(χ2981) → JM83 with sel'n for Tc ^r Asd ⁻
χ6097	K-12/F ⁻	<i>ara</i> Δ[<i>lac-pro</i>] <i>rpsL ΔasdA4</i> Δ[<i>zhf-2::Tn10</i>] <i>thi ø80dlacZ</i> Δ <i>M15</i>		FA ^r Tc ^s derivative of χ6096

<u>Strain number</u>	<u>Parent strain/ plasmid</u>	<u>Relevant genotype</u>	<u>Derivation</u>
χ 6212	K-12/F ⁻	$\Delta glnV44$ [<u>lacZYA-argF</u>][U169 λ Ø80d <i>lacZ</i> Δ M15 <i>gyrA</i> <i>recA1</i> <i>relA1</i> <i>endA1</i> Δ <i>asdA44</i> Δ [<i>zhf-2</i> ::Tn10] <i>hsdR17</i>	DH5 α
Y1090	K-12/F ⁻	Δ <i>araD139</i> Δ <i>lacU169</i> Δ <i>lon</i> <i>tyrT</i> <i>trpC22</i> ::Tn10 <i>rpsL</i> <i>hsdR</i> (pBR322 <i>lacP</i>) <i>thr-1</i> <i>lenB6</i> <i>lacY1</i> <i>recA</i> RP4-2-Tc::Mu λ <i>pir</i> Δ <i>asdA4</i>	Promega Biotech Sm10 λ <i>pir</i>
MGN-617	K-12/F ⁻		
<u>B. Salmonella typhimurium strains</u>			
χ 3000	LT2-Z/ pStLT100	prototroph, suppressor-free	Curtiss collection
χ 3008	LT2-Z/ pStLT100	<i>asdA15</i>	HNO ₂ -induced Asd ⁻ mutant of χ 3000
χ 3013	LT2-Z/ pStLT100	<i>zhf-1</i> ::Tn10	from P22(χ 3000::Tn10 library) \rightarrow χ 3008 with sel'n for Tc ^r Asd ⁺
χ 3021	LT2-Z/ pStLT100	Δ [<i>zhf-1</i> ::Tn10] Δ <i>asdA1</i> P22 ⁺	FA ^r Tc ^s derivative of χ 3013
χ 3385	LT2-Z/ pStLT100	<i>hsdL6</i> <i>galE596</i> <i>trpB2</i> <i>flaA66</i> <i>his-6165</i> <i>rpsL120</i> <i>xyl-404</i> <i>metE551</i> <i>metA22</i> λ amB ⁺ (<i>E. coli</i>) Δ <i>zja</i> ::Tn10 <i>hsdSA29</i> <i>val</i> Δ <i>asdA1</i> <i>zhf-4</i> ::Tn10	cured derivative of AS68 (E.T. Palva)
χ 3520	LT2-Z/ pStLT100		P22HTint(χ 3536) \rightarrow χ 3021 with sel'n for Tc ^r (<i>asd</i> ^r); P22HTint(χ 3021 Tc ^r <i>asd</i> ^r) ^a \rightarrow χ 3000 with sel'n for Tc ^r (Asd ^r)

<u>Strain number</u>	<u>Parent strain/ plasmid</u>	<u>Relevant genotype</u>	<u>Derivation</u>
$\chi 3536$	LT2-Z/ pStLT100	<i>zhf-4::Tn10</i>	from P22HTint($\chi 3324::Tn10$ library) \rightarrow $\chi 3000$; P22HTint($\chi 3000::Tn10$ library) \rightarrow $\chi 3021$ with sel'n for Tc ^r Asd ⁺ ; P22HTint($\chi 3021$ Tc ^r) ^a \rightarrow $\chi 3000$ with sel'n for Tc ^r
$\chi 3537$	LT2-Z/ pStLT100	<i>zhf-3::Tn10</i>	from P22HTint($\chi 3324::Tn10$ library) \rightarrow $\chi 3000$; P22HTint($\chi 3000::Tn10$ library) \rightarrow $\chi 3021$ Tc ^r ^a \rightarrow $\chi 3000$ with sel'n for Tc ^r
$\chi 3628$	LT2-Z/ pStLT100	$\Delta[zhf-3::Tn10] \Delta asdA13$	FA ^r Tc ^s Asd ^r derivative of $\chi 3537$
$\chi 3629$	LT2-Z	<i>hsdL6</i> $\Delta[galE-uvrB]-1005 flaA66$ <i>rpsL120 zhf-3::Tn10 xyl-404</i> lamB ⁺ (<i>E. coli</i>) $\Delta[zja::Tn10]$ <i>hsdSA29</i>	P22HTint($\chi 3537$) \rightarrow $\chi 3477$ with sel'n for Tc ^r Asd ⁺
$\chi 3630$	LT2-Z	<i>hsdL6</i> $\Delta[galE-uvrB]-1005 flaA66$ <i>rpsL120</i> $\Delta asdA13$ <i>xyl-404</i> lamB ⁺ (<i>E. coli</i>) $\Delta[zja::Tn10]$ <i>hsdSA29</i>	P22HTint($\chi 3628$) \rightarrow $\chi 3629$ with sel'n for Fa ^r Asd ⁺
$\chi 3638$	LT2-Z	<i>hsdL6</i> $\Delta[galE-uvrB]-1005 flaA66$ <i>rpsL120 zhf-4::Tn10 xyl-404</i> lamB ⁺ (<i>E. coli</i>) $\Delta[zja::Tn10]$ <i>hsdSA29</i>	P22HTint($\chi 3536$) \rightarrow $\chi 3477$ with sel'n for Tc ^r Asd ⁺
$\chi 3656$	LT2-Z/ pStLT100	<i>leu hsdLT galE trpD2 rpsL120</i> $\Delta asdA1 zhf-4::Tn10 metE551$ <i>metA22 hsdSA hsdSB ilv</i>	P22HTint(X3520) \rightarrow $\chi 3179$ with sel'n for Tc ^r Asd ⁺
$\chi 3761$	UK-1	prototroph	Curtiss et al. (1991)

<u>Strain number</u>	<u>Parent strain/ plasmid</u>	<u>Relevant genotype</u>	<u>Derivation</u>
χ 4064	SR-11/ pStSR100	<i>gyrA1816</i> Δ <i>cya-1</i> Δ <i>crp-1</i>	FA' Tc ^s derivative of χ 4055 (Curtiss and Kelly, 1987)
χ 4070	SR-11/ pStSR100	<i>gyrA1816</i> Δ <i>cya-1</i> Δ <i>crp-1</i> Δ <i>asdA1</i> <i>zlf-4::Tn10</i>	P22HTint(χ 3520) \rightarrow χ 4064 with sel'n for Tc' Asd'
χ 4072	SR-11/ pStSR100	<i>gyrA1816</i> Δ <i>cya-1</i> Δ <i>crp-1</i> Δ <i>asdA1</i> Δ [<i>zlf-4::Tn10</i>]	FA' Tc ^s derivative of χ 4070
χ 4550	SR-11/ pStSR100	<i>gyrA1816</i> Δ <i>asdA1</i> Δ [<i>zlf-2::Tn10</i>]	P22HT int (χ 3520) \rightarrow
χ 8315	UK-1	Δ <i>crp-1</i> Δ <i>cya-1</i>	χ 4064 followed by sel'n for FA' TC ^s (Asd')
DB9031	LT2-Z/ pStLT100	Δ <i>phoPQ23</i> Δ <i>asdA20::xylE</i>	MGN-762
MGN-023	UK-1	<i>zeh-4::Tn10</i>	Tn10 95% linked to <i>gyrA</i>
MGN-762	HK-1	Δ <i>asdA16</i>	χ 3761
MGN-1036	UK-1	Δ <i>phoPQ23</i>	χ 3761
		Δ <i>poxA270</i>	χ 3761

^aSince χ 3021 is lysogenic for P22, P22 HT int was propagated on the χ 3021 rtransductant following UV-induction (15 sec at 5 J/m²) of the prophage. The resulting lysate was used to transduce χ 3000.

Standard mutagenesis and mutant enrichment protocols are not efficient for the recovery of *asd* mutants, since desired mutants (requiring DAP) undergo lysis and death in the absence of DAP. Thus, previously isolated *asd* mutants were discovered indirectly and by chance, or by brute-force screening of millions of potential mutants. The invention

5 encompasses an efficient procedure for the selective enrichment and isolation of *asd* mutants.

In a synthetic medium, *asd* mutants require L-methionine, L-threonine, and DAP for growth. The requirement for L-methionine and L-threonine is satisfied by homoserine, which is a common precursor to both methionine and threonine (see Figure 1). Mutagenesis of an *E. coli* or *S. typhimurium* strain followed by an ampicillin-cycloserine procedure for the

10 enrichment of auxotrophic mutants seldom, if ever, recovers mutants with a sole requirement for homoserine. Curtiss et al (1965) describe a cycloserine-enrichment procedure for selecting auxotrophs, and a modification of that procedure also employing ampicillin is included in the Examples of U.S. Pat. 5,672,345. The reason that homoserine-requiring auxotrophs are seldom isolated is that β -aspartate semialdehyde is converted to homoserine

15 by either of two dehydrogenases which are encoded in two genes. The probability of inactivating both genes in a single cell is exceedingly small, and thus the homoserine-requiring auxotrophs may not be detected by random screening techniques.

This problem is overcome by the discovery that the inclusion of DAP in all media during mutagenesis, and enrichment or selection using the ampicillin-cycloserine technique,

20 leads to the recovery of *asd* mutants that require both homoserine and DAP. Ampicillin and cycloserine both inhibit cell wall synthesis in growing cells capable of protein synthesis, but are without effect on auxotrophic mutants unable to synthesize proteins because of the absence of nutritional requirements. The *asd* mutant strains χ 3008 and χ 2108 (see Table 1), which are *S. typhimurium* and *E. coli* strains, respectively, were isolated using this procedure.

25 The Asd^- phenotype of χ 3008 is due to a point mutation in the *asd* gene, and thus the frequency of reversion to Asd^+ is fairly high. On the other hand, the Asd^- phenotype of χ 2108 results from a deletion in the *asd* gene resulting in an undetectable reversion frequency.

Strains carrying mutations of the *asd* gene, particularly desirable deletion mutations, can be generated by techniques utilizing transposons as described in U.S. Patent 5,672,345.

30 Transposons can be added to a bacterial chromosome at many points. The characteristics of transposon insertion and deletion have been reviewed in Kleckner (1977). For example, the transposon Tn10, which confers resistance to tetracycline (and sensitivity to fusaric acid) can be used to create Δ *asd* mutants in a variety of bacterial species, including, for example, *E. coli* and *S. typhimurium* (EPO Pub. No. 315,682; U.S. Patent Nos. 5,387,744; 5,672,345).

One method for creating Δasd mutants in *E. coli* and *S. typhimurium* is described in the Examples of U.S. Pat. 5,672,345. First, a library of random Tn10 insertions in the chromosomes of the bacteria is created utilizing an appropriate transposon vector, for example, λ NK561 for *E. coli* (Kleckner et al., 1977) with a λ -sensitive strain of *S.*

5 *typhimurium*, an example of which is χ 3385 (Table 1). A suitable transducing phage, for example, PIL4 or P22HT *int*, for *E. coli* and *S. typhimurium*, respectively, which has been propagated on the Tn10 library in the appropriate species, is used to transduce Asd⁺ mutants of that species, and bacteria containing an Asd⁺ Tc^r phenotype are selected. Examples of useful Asd⁺ strains are the *E. coli* strain χ 2108, and the *S. typhimurium* strain χ 3008 (see Table
10 1). Since single events are more probable than double events, most transductants, for example χ 2978 and χ 3013 (see Table 1) will have Tn10 closely linked to the *asd* gene. Selection for fusaric acid resistance, which results from deletion of Tn10 and adjacent DNA sequences, yields Δasd mutants in which all or portions of the closely linked *asd* gene have been deleted. The $\Delta asdA1$ mutation in the *S. typhimurium* χ 3021 strain was isolated from
15 χ 3013 (Table 1) using this procedure.

Deletion mutations can also be introduced into the bacterial chromosome by using recombinant DNA techniques. For example, a specific portion of the *asd* gene can be deleted from pYA272 or similar plasmid, and the derived plasmid introduced into an Asd⁺ *S.*
20 *typhimurium* strain to allow for homologous recombination leading to cells that have the genetically engineered Δasd mutation in the chromosome as well as in the plasmid. The culture is then grown at elevated temperatures, for example, 43° C, in the presence of low concentrations of novobiocin, plated on medium devoid of antibiotics, and then replica plated to medium containing ampicillin to identify clones that have lost the recombinant plasmid derived from pUC18, which confers resistance to ampicillin. See, e.g., Example 17 of U.S.
25 Pat. 5,672,345, describing the cloning of the *asd* gene of *S. typhimurium* into pUC18 to yield pYA272 following subcloning and transposon mutagenesis to delimit the extent of the *S. typhimurium asd* gene in pYA275.

Generation of defined deletion (Δ) mutations may be facilitated by using a *pir*-dependent R6K replicon (Miller and Mekalanos, 1988) where the suicide vector is unable to
30 replicate in a cell lacking the *pir* gene, which is inserted into the chromosome of the donor parent. Selection for allele replacement in the recipient bacterium is enhanced by use of sucrose selection since the *sacB* gene present on the *pir*-dependent suicide vector confers sucrose sensitivity to cells that possess the gene (Kaniga et al, 1991). In this case, following a single crossover event to integrate the suicide vector into the chromosome, plating on agar
35 medium in the presence of 5% sucrose selects for loss of the integrated suicide vector, which

sometimes will occur by a second recombination event such that the deletion mutation on the original suicide vector replaces the wild-type gene in the chromosome.

When the desired double crossover event to generate a Δasd strain is sufficiently frequent, direct screening for the nutritional requirement imposed by the deletion mutation is a relatively efficient screening process. This screening process can be simplified by the insertion into the defined deletion a reporter gene that would be expressed and recognized by spraying colonies with a chromogenic substrate. Such a construction would also facilitate studies to examine the genetic stability of strains with various deletion mutations in the native essential gene when possessing extrachromosomal vectors that could permit homologous recombination to replace the mutated essential gene with the wild-type complementing gene on the plasmid vector. Such studies are important in validating the utility of a functional balanced-lethal host-vector system when employed for production of products by fermentation or use as vaccines for immunization of animals and humans. A useful gene for this purpose is the *xyIE* reporter gene (Kaniga et al., 1994) since colonies on an agar plate can be sprayed with a 250 mM catechol solution. Colonies that express the *xyIE* gene will turn yellow in about five minutes and the spray does not effect the viability of cells within the colony.

After isolating and characterizing a deletion mutant, it may be advantageous to place a transposon such as *Tn10* adjacent to the deletion, by well-known methods, so that the deletion can be moved into other strains. For example, the *zhf-2::Tn10* insertion in the *E. coli* K-12 strain $\chi 6096$ (Table 1) can be transduced using standard transduction procedures for P1L4 to introduce the transposon into a great diversity of bacterial strains and species that are transducible with the wide host range generalized transducing phage P1L4. Since tetracycline resistance is associated with sensitivity to fusaric acid, one can take a P1L4 lysate grown on a strain carrying a Δasd mutation, for example, $\chi 2984$ (Table 1) and transduce any recipient strain with a construct such as *zhf-2::Tn10*, followed by selection for fusaric acid resistance. In this case, the Δasd mutation replaces the *zhf-2::Tn10*. If the recipient strain has a different restriction behavior than *E. coli* K-12, subjecting the recipient strain to a brief heat shock, for example, 5 to 10 min at 45°- 50° C, may eliminate this barrier.

An analogous method can be used for isolating Δasd mutants of various strains of *S. typhimurium*. The generalized transducing phage P22HT *int* can be grown on strains such as, for example, $\chi 3013$, $\chi 3536$, or $\chi 3537$, which possess *zhf-1::Tn10*, *zhf-4::Tn10*, and *zhf3::Tn10*, respectively (see Table 1). The phage carrying the transposon is then used to transduce other suitable recipient strains to tetracycline resistance. A P22HT *int* lysate, resulting from propagation of the phage on a bacterial strain carrying a Δasd mutation, for

example χ 3021 or χ 3628, is used to transduce a strain carrying a *zhf::Tn10* insertion.

Mutants that are resistant to fusaric acid are selected. As with *E. coli*, the Δasd mutation replaces the inserted *Tn10*.

It should be noted that transduction to insert Δasd mutations as replacements for a *zhf::Tn10* insertion, with selection of the desired transductant by its resistance to fusaric acid occurs at a frequency of 10^{-4} - 10^{-5} , whereas spontaneous loss of the *Tn10* insert by a deletion type mutational event occurs at a frequency of about 10^{-8} . Thus, the use of transduction with a phage carrying a Δasd gene in the construction of the desired strains ensures the correct genotype with a very low probability for recovery of new deletion mutants.

Many strains of *Salmonella* are not transducible with phage P22. For example, two of the *Tn10* insertions linked to the *asd* gene, the $\Delta asdA13$ mutation and the $\Delta asdA4$ mutation linked to *zhf-4::Tn10* may be placed in *Salmonella* strains that possess a *galE* mutation. When these strains, χ 3629, χ 3638, χ 3630 and χ 3656, respectively, are grown in the presence of galactose they have a normal smooth lipopolysaccharide coat (LPS) and are sensitive to P22. However, growth in the absence of galactose causes the cells to have a rough coat lacking LPS side chains. Those cells are infectible by P1L4. P1L4 can be propagated on χ 3629 (Table 1), and the lysate used to transduce a P1L4 sensitive strain, resulting in a *zhf-3::Tn10* insertion into the strain. P1L4 propagated on χ 3630, which has the $\Delta asdA13$ mutation, is used to transduce the *Tn10* carrying strain, and fusaric acid resistant cells are selected. The result is the introduction of the $\Delta asdA13$ mutation into a new *Salmonella* strain. Alternatively, P1L4 can be propagated on χ 3656 and a suitable recipient transduced to Tc^r in the presence of DAP. In this way the $\Delta asdA4$ mutation can be inherited linked to *zhf4::Tn10*. The *zhf-4::Tn10* can then be removed by transduction with P1L4 grown on χ 3385 (Table 1) and used to transduce to Tc^s by selecting for fusaric acid resistance.

If transduction of one of the available *asd* deletion mutations into a species or strain of choice is not feasible or possible, then the strategy previously described for isolation of *asd* mutants can be employed. A bacterial strain is mutagenized, and mutant enrichment and selection is carried out in the presence of DAP to selectively isolate mutants unable to synthesize homoserine. After obtaining an *asd* mutation, the reversion frequency of the mutant is determined. If a deletion mutation is desired, it can be done in a variety of ways known in the art, but most simply by introducing a *Tn10* transposon library by transduction, selecting for a simultaneous Asd^+ and Tc^r phenotype. Generally, the *Tn10* will be closely linked to the *asd* gene, and if fusaric acid resistant isolates are selected, deletion of the *Tn10* and the adjacent DNA into the *asd* gene will result in an *asd* deletion mutation. If the *Tn10* procedure does not provide results in a bacterial species, then another transposon can be used

to establish linkage to the *asd* gene; available transposons are known in the art (see Berg & Howe (1989); Craig NL, Chapter 124 in Neidhardt et al. (1986)). The transposon-*asd* gene complex can be cloned using known genetic engineering techniques. A recombinant can be prepared with precise deletion of the *asd* gene, the deleted *asd* gene can then be returned to the wild-type bacterial strain, as described above.

Alternatively, a defined deletion mutation can be generated within a cloned gene sequence using standard molecular genetic manipulations with restriction enzymes and subcloning or by using polymerase chain reaction (PCR) procedures. A mutated allele with a defined deletion can then be introduced into a *pir*-dependent R6K suicide vector with the *sacB* genetic determinant conferring sucrose sensitivity and allele replacement selected after transfer of the suicide vector, either by electroporation or conjugation, into the recipient strain of bacteria desired to be mutated.

Another characteristic of the host cells of the invention is that they comprise two recombinant genes. The first recombinant gene, the "complementing gene" or "complementing recombinant gene" or "complementing essential gene" encodes a polypeptide that functionally replaces the enzymatic activity of the inactive native essential gene. For example, an *Asd⁻* *E. coli* cell may be transformed with a recombinant polynucleotide construct encoding the *asd* gene from *S. mutans*. See Curtiss et al (1982) for evidence that the *S. mutans asd* gene product functionally replaces the *E. coli* gene product.

The above *E. coli* cells comprising the *S. mutans asd* complementing essential gene exemplifies another characteristic of the complementing essential gene that is considered desirable, that it does not undergo homologous recombination with the mutant *E. coli* essential gene because of a lack of sequence homology. The *S. mutans asd* gene sequence, and its lack of homology to the *E. coli* sequence is reported in Cardineau and Curtiss (1987). The lack of recombination between the host cell gene and the recombinant gene is useful for maintaining the linked selective pressure for the second recombinant gene. One can, however, avoid homologous recombination while using a complementing gene cloned from the desired recipient strain provided that the recipient host has some or all of the nucleotide sequence of the native essential gene and/or flanking sequences deleted so that double crossover recombination with the cloned *asd* gene in the vector is not possible. Examples of such combinations of a mutant native essential gene and a complementing recombinant essential gene include the *S. typhimurium asd* gene as contained in the vector pYA292 with mutant *asd* genes contained in a variety of *E. coli* and/or *S. typhimurium* strains with Δasd strains which lack any and all nucleotide sequences contained on pYA292; and a system in which the deletion is partial for the *asd* structural gene, but extends into its flanking regions.

Pat. 5,672,345, and includes pYA248. Table 1 lists bacterial strains and Table 2 lists strains and plasmids for plasmid constructions.

Table 2

Plasmids

<u>Plasmid</u>	<u>Property</u>	<u>Derivation</u>	<u>Host strain number</u>	<u>Relevant genotype</u>
F(<i>traD36</i> proA ⁺ proB ⁺ lacI ^q ΔM15) pSGMU37	7.6kb, LacZ ⁺	Errington (1986)	χ6054	<i>recA1</i> Δ(<i>lac-pro</i>) <i>endA1</i> <i>gyrA96</i> <i>endA1</i> <i>gyrA96</i> <i>thi-1</i> <i>hsdR17</i> <i>supE44</i> <i>relA1</i>
pMEG-006	3.88kb, MCS, <i>tetR</i> , <i>tetA</i> , Δ <i>asdA16</i>	See Example 1	MGN-617	see Table 1
pMEG-223	8.4kb, <i>sacR</i> , <i>sacB</i> , Δ <i>asd20</i> , <i>xyIE</i>	See Example 2	MGN-617	see Table 1
pMEG-443	9.7kb, MCS, cat, amp, <i>sacR</i> , <i>sacB</i> , Δ <i>asdA16</i>	See Example 1	MGN-617	see Table 1
pVAX1-asd	3.7kb, SD- <i>asd</i> , P _{CMV} , MCS	See Example 6	χ4072	see Table 1
pYA248	3.0kb, P _{trc} promoter, MCS	U.S. Pat. 672,345	χ4072	see Table 1
pYA261	SpaA	U.S. Pat. 672,345	χ4072	see Table 1
pYA262	SpaA	U.S. Pat. 672,345	χ4072	see Table 1
pYA280	4.45kb, MCS, Ap ^r , <i>asd</i> ⁺	See Example 18 of U.S. Pat. 5,672,345	χ6097	see Table 1
pYA292	3.9kb, P _{trc} promoter, MCS, <i>lacZ</i> (α), <i>asd</i> ⁺ , <i>rrnB</i> transcription terminator	See Example 19 of U.S. Pat. 5,672,345	MGN-617	see Table 1
pYA810	3.15kb, P _{trc} promoter, MCS, <i>lacZ</i> (α), <i>asd</i> ⁺ , <i>rrnB</i> transcription terminator	See Example 3		see Table 1

<u>Plasmid</u>	<u>Property</u>	<u>Derivation</u>	<u>Host strain number</u>	<u>Relevant genotype</u>
pYA3137	3.5 <i>asd</i> ⁺ , MCS pUC ori	See Example 4	MGN-023	
pYA3149	3.7 <i>asd</i> ⁺ , MCS pBR322 ori	See Example 4	MGN-0223	
pYA3332	3.3kb, <i>asd</i> ⁺ , MCS, p15A ori	See Example 3	MGN-023	see Table 1
pYA3333	3.5kb, <i>asd</i> ⁺ , MCS, pBR ori	See Example 3	MGN-023	see Table 1
pYA3334	3.4kb, <i>asd</i> ⁺ , MCS, pUC ori	See Example 3	MGN-023	see Table 1
pYA3341	2.6kb, <i>asd</i> ⁺ , MCS, pUC ori, P _{trc} promoter	See Example 4	MGN-023	see Table 1
pYA3342	2.8kb, <i>asd</i> ⁺ , MCS, pBR ori, P _{trc} promoter	See Example 4	MGN-023	see Table 1

As established herein, host cells of the present invention may also have defined chromosomal deletions of the native essential gene with small regions of homologous DNA sequences in the vector-borne complementing recombinant gene. This could permit either single homologous recombination events or separate homologous recombination events on either side of the inactive native gene. Such events would result in restoration of the chromosomal DAP-prototrophic phenotype due to the presence of copies of the complementing gene present on the chromosome, as well as on the plasmid vector. Even though such recombination events can be theoretically possible, it is established herein that they generally occur at a sufficiently low frequency as to be undetectable. They could possibly be detectable only after long periods of time of the recombinant strains in an immunized animal host or following growth in culture for an excess of 50 generations. In these instances, the utility of the invention is as good as in constructions in which recombination to replace the mutated chromosomal gene is not possible because of a complete absence of nucleotide sequence homology between the plasmid and the chromosome. See, e.g., Example 5, showing that the presence of such regions of homology does not result in detectable loss of expression of the desired gene.

All the genes involved in the biosynthesis of DAP are located in the chromosome and are presumably regulated to some extent by the required amount of DAP needed to support cell wall synthesis which is dependent upon growth rate and conversion to lysine required for protein synthesis. When the gene for one of the enzymes in this pathway is located on a multicopy extrachromosomal vector, as is the complementing recombinant gene of the present invention, it can be expected that the production of that essential enzyme will be far in excess of what is needed to catalyze the required biosynthetic step in the synthesis of DAP. Since the level of enzyme synthesized is more or less proportional to gene copy number, it can be expected that bacterial cells containing such an extrachromosomal vector would produce excess essential enzyme equivalent to the copy number of the vector. For example, the pYA3332 vector (Figure 8) with its p15A replicon discussed in Example 3 would have 15 to 20 times more Asd protein than necessary. Similarly, the cells with the pYA3333 and pYA3334 Asd⁺ plasmids (Figure 8) would be expected to synthesize an even greater excess of the Asd protein. Since the overexpression of proteins is of no benefit to a cell and places energy demands for the synthesis of this excess protein on the cell, slower growth results. Thus, the bacterial strain would have a poorer performance when used for any of the potential applications in which a functional balanced-lethal host-vector system would be employed. Therefore, the present invention contemplates the use of origins of replication in the extrachromosomal vectors that result in high copy number of the vector, providing for high

expression of the desired gene, but in which expression of the *asd* gene is reduced, maximizing viability of the host cells. Such constructs are within the skill of the art. Example 4 provides examples of how this can be accomplished. As described therein, eliminating the -35 and -10 promoter sequences for the *asd* gene still provides for sufficient

5 production of Asd to maintain viability, since sufficient *asd* mRNA is made by occasional accidental transcription of the *asd* gene by one or more of the 100 or more plasmid copies present in each cell. Translation of that rare *asd* mRNA yields just enough Asd enzyme to catalyze the synthesis of a sufficient amount of DAP for cell wall synthesis.

As previously discussed, the host cells of the present invention also have a desired

10 recombinant gene encoding the polynucleotide of a desired gene product such as a polypeptide or a mRNA. The choice of desired gene is not narrowly limited and may include any gene useful in a vaccine, including genes encoding, for example, viral, bacterial, fungal or parasite antigens, cytokines or lymphokines, etc. In preferred embodiments, the expression of the desired gene is dependent on a control sequence linked to the recombinant complementing

15 essential gene. For example, in pYA261 and pYA262 of Example 13 of U.S. Patent 5,672,345, the desired gene *spaA* is controlled by the P_{trc} promoter. Preferably, the desired gene and the complementing gene are on the same extrachromosomal vector (e.g., plasmid). In this way, loss of the desired gene due to the loss of the extrachromosomal vector will result in lysis of the cell because the complementing gene (encoding an enzyme required for cell

20 wall synthesis) will be lost. Methods of constructing vectors with these characteristics are known in the art using recombinant DNA technology and are discussed more fully in the section on vaccines, infra. See also, e.g., U.S. Patents 4,190,495; 4,424,065; 4,888,170; 5,294,441; 5,389,368; 5,468,485; 5,656,488; 5,672,345 5,840,483; 5,855,879; 5,855,880; and 6,024,961. Examples of vectors in which the second gene encodes β -galactosidase, surface

25 protein antigen A (SpaA) of *S. mutans*, and antigens from *M. leprae* are presented in U.S. Patent 5,672,345. However, the choice of the desired gene is not limited to any particular encoded polypeptide that can be produced in the host cell. Included in the Examples section and in U.S. Pat. 5,672,345 are expression vectors, generally suitable for insertion of any desired gene by known methods, which contain the *S. mutans asd* gene or the *S. typhimurium*

30 *asd* gene, which are useful for complementing the Asd⁻ phenotype in *S. typhimurium* and in *E. coli*.

In order for the desired gene to be useful in the present invention, the gene must be expressed. Gene expression means that the information encoded in the sequence of DNA bases is transformed into a physical product in the form of a RNA molecule, polypeptide or

35 other biological molecule by the biochemical mechanisms of the cell in which the gene is

located. The biological molecule so produced is called the gene product. The term gene product as used here refers to any biological product or products produced as a result of expression of the gene. The gene product may be, for example, an RNA molecule, a peptide, or a product produced under the control of an enzyme or other molecule that is the initial product of the gene, i.e., a metabolic product. For example, a gene may first control the synthesis of an RNA molecule that is translated by the action of ribosomes into an enzyme that controls the formation of glycans in the environment external to the original cell in which the gene was found. The RNA molecule, the enzyme, and the glycan are all gene products as the term is used here. Any of these as well as many other types of gene products, such as glycoproteins and polysaccharides, will act as antigens if introduced into the immune system of an animal. Protein gene products, including glycoproteins and lipoproteins, are preferred gene products for use as antigens in vaccines.

The above-described balanced-lethal host vectors are useful as constituents of live vaccines. In these cases, the desired recombinant gene would encode an antigen of a fungal, bacterial, parasitic, or viral disease agent. Live vaccines are particularly useful where localized immunity to the disease agent is important and might be a first line of defense.

The host cells used in live vaccines are attenuated derivatives of pathogens. Most preferably, the attenuated derivatives are able to attach to, invade and persist in the gut-associated lymphoid tissue (GALT) or bronchial-associated lymphoid tissue (BALT). Such attenuated host cells are preferred because they are known to be able to persist in the inoculated animal, causing exposure to the antigen for an extended time period. Such a long exposure period is known to be highly effective in inducing an immunogenic response to the antigen.

Attenuation can be conferred upon the microbes by any known means, including chemical mutagenesis and the use of various recombinant genes. Preferred methods of conferring attenuation render the host cells unable to revert to the virulent condition. The most preferred methods of conferring attenuation on host cells are through the introduction of stable mutations or gene insertions by recombinant methods. Non-limiting examples of such methods include (1) introducing mutations that impose a requirement for aromatic amino acids and vitamins derived from precursors in this pathway (Stocker et al., 1983, *Dev. Biol. Stand.* 53:47-54; Hoiseth and Stocker, 1981, *Nature* 291:238-9); (2) mutating genes for global regulators such as *cya* and *cyp* (U.S. Patents 5,389,368; 5,855,879; 5,855,880; 5,294,441 and 5,468,485), *phoP* (U.S. Patent 5,424,065), *ompR* (Dorman et al., 1989, *Infect. Immun.* 57:2136-40), and *poxA* (Kaniga et al.(1998)); (3) mutating genes for lipopolysaccharide (LPS) synthesis, such as *galE* (Germanier et al., 1975, *J. Infect. Dis.* 131:553-8), although this alone

may be insufficient (Hone et al., 1988, *Infect. Immun.* 56:1325-33); (4) mutating genes needed for colonization of deep tissues, such as *cdt* (U.S. Patent 5,387,744); or (5) by preventing expression of genes for proteases required at high temperature, such as *htrA* (Johnson et al., 1991, *Mol. Microbiol.* 5:401-7).

5 Once rendered attenuated, the microbes can serve as the immunogenic component of a vaccine to induce immunity against the microbe. Thus, the use of any microbe possessing the characteristics of the host cells described supra, including non-pathogenicity, are contemplated by this invention, including but not limited to *E. coli*, *Salmonella spp.*, *E. coli - S. typhimurium* hybrids, *Shigella spp.*, *Yersinia spp.*, *Pasteurella spp.*, *Legionella spp.* or *Brucella spp.* Preferred microbes are members of the genus *Salmonella* such as *S. typhimurium*, *S. typhi*, *S. paratyphi*, *S. gallinarum*, *S. enteritidis*, *S. choleraesuis*, *S. arizonae*, or *S. dublin*.

In certain embodiments of the invention, the attenuated derivative of a pathogenic microbe (also referred to herein as a carrier bacterium) can be used to deliver selected antigens to the GALT, for example to the Peyer's patches of the ileum. Some genera of bacteria, such as *Salmonella*, are known to home to the Peyer's patches (Carter et al., 1974, *J. Exp. Med.* 139:1189). Also, *S. typhimurium*-*E. coli* hybrids have also been shown to colonize Peyer's patches in mice (Hohmann, A.W., et al, 1978, *Infect. Immun.* 22:763). By engineering these carrier bacteria to contain and express a recombinant desired gene encoding an antigen from a pathogenic organism, antibodies will be produced against the desired gene product from the pathogen as described in U.S. Pat. No. 5,888,799. As is well known, recombinant DNA techniques now allow the development of totally unique vaccines in which specific antigens are produced by another host strain of bacteria capable of expressing the gene for that antigen. It is also possible, when antigens might cross-react with an antigen of the mammalian host and thus potentiate the induction of autoimmunity, to use recombinant DNA techniques to alter the gene so that the affecting cross-reacting antigenic determinant is not produced. Thus, recombinant DNA techniques can be employed to develop vaccines that do not have any material capable of cross-reacting with vertebrate host antigens or capable of eliciting an autoimmune state.

Thus, the present invention has wide applicability to the development of effective vaccines against bacterial, fungal, parasite or viral disease agents, in which local immunity is important and might be a first line of defense. Nonlimiting examples are vaccines for the control of pneumonic plague caused by *Yersinia pestis*, of gonorrhea caused by *Neisseria gonorrhoeae*, of syphilis caused by *Treponema pallidum*, and of venereal diseases as well as eye infections caused by *Chlamydia trachomatis*. Species of *Streptococcus* from both group

A and group B, such as those species that cause sore throat or heart diseases, *Neisseria meningitidis*, *Mycoplasma pneumoniae*, *Hemophilus influenza*, *Bordetella pertussis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Bordetella avium*, *Escherichia coli*, *Streptococcus equi*, *Streptococcus pneumoniae*, *Brucella abortus*, *Pasteurella hemolytica*,
 5 *Vibrio cholera*, *Shigella spp.*, *Legionella pneumophila*, and other pathogenic bacteria of the genera of the above organisms are additional, nonlimiting examples of bacteria within the scope of this invention from which genes could be obtained. Viral vaccines, such as those produced against influenza viruses, are also encompassed by this invention. Viral vaccines can also be produced against other viruses, either DNA or RNA viruses. Non-limiting
 10 examples include viruses from the classes Papovirus, Adenovirus, Herpesvirus, Poxvirus, Parvovirus, Reovirus, Picornavirus, Myxovirus, Paramyxovirus, Flavivirus or Retrovirus. Vaccines to protect against infection by pathogenic fungi, protozoa and parasites are also contemplated by this invention.

In an additional embodiment, the invention encompasses a vaccine for the
 15 immunization of a vertebrate animal. The vaccine comprises a live attenuated derivative of a pathogenic microbe, wherein the derivative is substantially incapable of producing functional adenylate cyclase and AMP receptor protein while being capable of expressing a recombinant gene derived from an organism that is a pathogen of or that produces an allergen of said animal. See, e.g., Valenta et al, *Allergy* 53:552-561. 1998; Olsson et al., *Clin. Exp. Allergy*
 20 28:984-991. 1998; Soldatova et al., *J. Allergy Clin. Immunol.* 101:691-698, 1998; Twardosz et al, *Biochem Biophys Res Commun* 239:197-204, 1997.

In order for a vaccine to be effective in inducing antibodies, the antigenic material must be released in such a way that the antibody-producing mechanism of the vaccinated animal can come into play. Therefore the microbe carrier of the gene product must be
 25 introduced into the animal. In order to stimulate a preferred response of the GALT or BALT cells as discussed previously, introduction of the microbe or gene product directly into the gut or bronchus is preferred, such as by oral administration, gastric intubation or in the form of intranasal, although other methods of administering the vaccine, such as intravenous, intramuscular, subcutaneous injection or intramammary or intrapenial or vaginal
 30 administration, are possible.

When the attenuated microbe is used as a vaccine, the antigen needs to become available to the animal's immune system. This may be accomplished when the carrier microbe dies so that the antigen molecules are released. Of course, the use of "leaky" avirulent mutants that release the contents of the periplasm without lysis is also possible.

The use of the avirulent strain with *asd* mutations and occasional loss of the Asd⁺ cloning vector would permit lysis of approximately 1% of the bacteria during each generation (see examples) to release the cell contents to thus stimulate an immune response against the released cell contents including any colonization and virulence antigens.

Administration of a live vaccine of the type disclosed above to an animal may be by any known or standard technique. These include oral ingestion, gastric intubation, or broncho-nasal spraying. All of these methods allow the live vaccine to easily reach the GALT or BALT cells and induce antibody formation and are the preferred methods of administration. Other methods of administration, such as intravenous injection to allow the carrier microbe to reach the animal's blood stream may be acceptable. Intravenous, intramuscular or intramammary injection is also acceptable with other embodiments of the invention, as is described later.

The dosages required will vary with the antigenicity of the gene product and need
35 only be an amount sufficient to induce an immune response typical of existing vaccines.

Routine experimentation will easily establish the required amount. Typical initial dosages of vaccine could be 0.001-0.1 mg antigen/kg body weight, with increasing amounts or multiple dosages used as needed to provide the desired level of protection.

5 The pharmaceutical carrier in which the vaccine is suspended or dissolved may be any solvent or solid or encapsulated in a material that is non-toxic to the inoculated animal and compatible with the carrier organism or antigenic gene product. Suitable pharmaceutical carriers include liquid carriers, such as normal saline and other non-toxic salts at or near physiological concentrations, and solid carriers not used for humans, such as talc, sucrose, and feed for farm animals. Adjuvants may be added to enhance the antigenicity if desired.

10 When used for administering via the bronchial tubes, the vaccine is preferably presented in the form of an aerosol.

Immunization with a pathogen-derived gene product can also be used in conjunction with prior immunization with the attenuated derivative of a pathogenic microorganism acting as a carrier to express the gene product specified by a recombinant gene from a pathogen.

15 Such parenteral immunization can serve as a booster to enhance expression of the secretory immune response once the secretory immune system to that pathogen-derived gene product has been primed by immunization with the carrier microbe expressing the desired gene product to stimulate the lymphoid cells of the GALT or BALT. The enhanced response is known as a secondary, booster, or anamnestic response and results in prolonged immune

20 protection of the host. Booster immunizations may be repeated numerous times with beneficial results.

In other embodiments of the invention, a recombinant attenuated derivative of a pathogenic microbe can be used to express, in the animal host, gene products that are therapeutic against disease in the inoculated animal. Non-limiting examples of such products

25 include lymphokines or cytokines to modulate the immune response (Saltzman et al. (1996); Saltzman et al. (1997); Whittle et al. (1997); Dunstan et al. (1996)), sperm-specific and egg-specific autoantigens to arrest fertility (U.S. Patent No. 5,656,488), specific antibodies, e.g., which bind to tumors or pathogens such as viruses, fungi, parasites, or bacteria, or gene products essential for a pathogen to cause disease), or enzymes that have the potential to

30 convert prodrugs into toxic drugs within a tumor cell mass in an individual with a solid tumor (Pawelek et al. (1997)).

Because the avirulent microbes of this invention are able to traverse a variety of immunocompetent structures including the GALT, mesenteric lymph nodes and spleen, such microbes may also be used to modulate the immune system by producing a variety of

35 immunoregulatory products. Accordingly, one or more genes encoding immunoregulatory

immunoregulatory molecules include colony stimulating factors (macrophage, granulocyte, or mixed), macrophage chemotoxin, macrophage inhibition factor, leukocyte inhibitory factors, lymphotoxins, blastogenic factor, interferons, and interleukins.

20 Deposits of Strains Useful in Practicing the Invention

	<u>Strain</u>	<u>Deposit Date</u>	<u>ATCC No.</u>
35	χ 6097 containing pYA232	Oct. 6, 1987	67,537
	χ 2978	Oct. 6, 1987	53,679

	χ 3520	Oct. 6, 1987	53,681
	χ 4072 containing pYA248	Oct. 6, 1987	67,538
	χ 3008	Oct. 6, 1987	53,680
	χ 2108	Oct. 6, 1987	53,678
5	χ 6097 containing pYA292	Sept. 26, 1988	67,813

Preferred embodiments of the invention are described in the following examples. Other embodiments within the scope of the claims herein will be apparent to one skilled in the art from consideration of the specification or practice of the invention as disclosed herein. It is intended that the specification, together with the examples, be considered exemplary only, with the scope and spirit of the invention being indicated by the claims which follow the examples.

Examples

15

1. Generation of defined deletion (Δ) mutations in the *S. typhimurium asd* gene.

The complete nucleotide sequence of the *S. typhimurium asd* gene and flanking regions is presented in FIG. 2A (SEQ ID NO:1). This sequence includes the 244 bp upstream of the *asd* sequence, the *asd* ORF of 1176 bp, and a downstream sequence of 315 bp with start and stop sites indicated by bold letters. The amino acid sequence encoded by the ORF is indicated in FIG. 2B. In Example 6 of U.S. Pat. 5,672,345, we described a means to generate Δasd mutations by excision of a *Tn10* closely linked to the *asd* gene. The excision of the *Tn10*, selected for by selecting for fusaric acid resistance, leads to deletions of all or part of the *asd* gene and all DNA sequences between the *asd* gene and the site of the *Tn10* insertion. As a consequence, genetic information flanking the *asd* gene is deleted. This has the potential of attenuating the Δasd *Salmonella* strain even when an *Asd*⁺ plasmid vector is present. Such potential additional attenuation in conjunction with attenuation due to mutations, such as *cya* and *crp*, *phoPQ*, *aroA*, *C*, or *D*, etc. could result in hyperattenuation and thus reduce immunogenicity of the vaccine strain. Rather than having to contend with such possibilities, it is preferable to generate defined deletion mutations that only lack known DNA sequences that encode a desired gene and no more, in this case the *asd* gene. One method to generate the defined deletions of the *S. typhimurium asd* gene is as follows.

The 1.7 kb *Bgl*III fragment containing 1735 bp with the *asd* sequence depicted in FIG. 2B is cloned from pYA292 (Figure 16 of U.S. Pat. 5,672,345) into the *Bam*HI site of the *pir*-dependent suicide replicon pMEG-002 to generate pMEG-003. This particular suicide vector possesses the *tetA* and *tetR* genes conferring tetracycline resistance and confers sensitivity to fusaric acid upon cells possessing this plasmid. Inverse PCR on used on the sequence in

pMEG-003 so as to delete base pairs 219 through 1460 in the *asd* sequence (SEQ ID NO:1; depicted in FIG. 2A) and to insert in its stead a 6-base sequence encoding a *Bg*/III restriction enzyme cleavage site. The resulting plasmid pMEG-006 is depicted in Figure 3. The defined deletion mutation present in pMEG-006, if introduced into the chromosome of a recipient cell, would impose nutritional requirements for DAP and homoserine (or threonine and methionine). pMEG-006 is then introduced by electroporation into the suicide plasmid donor MGN-617 (Table 1) which possesses a *λpir* prophage to ensure faithful suicide plasmid replication. MGN-617 possesses a Δ *asd* mutation which can be used for counter-selection against the donor after transfer of the suicide vector into a desired recipient strain, usually a derivative of *S. typhimurium*. In such a mating, tetracycline-resistant DAP-independent isolates are selected which result from a single crossover to integrate pMEG-006 into the chromosome. These isolates are then grown up in L broth and fusaric acid-resistant isolates are selected in the presence of DAP. In some cases the second crossover, which is necessary to eliminate the integrated plasmid to confer fusaric acid resistance, will occur at a second site between the homologous sequences adjacent to the *asd* gene in the chromosome and the deleted *asd* sequence in pMEG-006, wherein this second recombination event occurs on the opposite side of the deleted *asd* sequence than was used for the first recombination event. This results in replacement of the wild-type *asd*⁺ allele in the chromosome for the Δ *asdA16* defined deletion allele present in the suicide vector. PCR is used to prove the existence of the Δ *asdA16* mutation.

Since the pMEG-006 suicide vector specifying tetracycline resistance, which necessitates fusaric acid selection to achieve allele replacement, does not always work efficiently, an additional suicide vector was constructed. This vector still has the *pir*-dependent R6K replicon, genes for ampicillin resistance and chloramphenicol resistance to ensure integration of the suicide vector into the chromosome of recipient strains, but has the *sacR* and *sacB* genes, conferring sensitivity to sucrose, to enable efficient selection for excision of the vector from the chromosome to achieve the second crossover event to generate the allele replacement. The vector pMEG-443 depicted in FIG. 4 was generated by excising the 1.5 kb *Hinc*II-*Sph*I fragment of pMEG-006 containing the Δ *asdA16* allele along with the R6K *ori* and inserting it into the *Sma*I and *Sph*I sites in the suicide vector pMEG-375. The pMEG-443 suicide vector was then introduced into the suicide vector donor strain MGN-617, which was then mated with the desired recipient strain. This was followed by selection for ampicillin and chloramphenicol resistance. Isolates resistant to ampicillin and chloramphenicol were purified, grown up in L broth, and then plated in the presence of 5% sucrose to select for a second crossover event, which sometimes occurs so that the Δ *asdA16*

5 2. Generation of a Defined Deletion Mutation Within the *S. typhimurium* *asd* Gene and
 Replacing it with a *xylE* Reporter Gene Identified by a Screen with a Chromogenic Substrate.

The $\Delta asdA20::xylE$ allele and flanking sequences was retrieved from pMEG-222 as a *Bgl*III-*Xba*I fragment which was then inserted into the *Bam*HI-*Xba*I sites of the sucrose-based suicide vector pKNG-101 (Kaniga et al., Gene 109:137-141,1991) to yield pMEG-223 which is depicted in FIG. 5. The suicide plasmid pMEG-223 was electroporated into the universal donor strain MGN-617. The $\Delta asdA20::xylE$ allele was introduced into the chromosome of several *S. typhimurium* strains including MGN-762 ($\Delta phoPQ23$), MGN-1036 ($\Delta pox A270$) and into other strains as listed in Table 1. The MGN-617 donor strain with pMEG-223 was grown over night in Luria broth, as was a recipient strain, such as the prototroph $\chi 3761$ (Table 1). Samples of donor and recipient over night cultures (100 μ l) were introduced into 5 ml BSG, filtered through a sterile 0.45 μ m Millipore filter and the filter aseptically placed on top of a Luria agar plate containing 100 μ g DAP/ml. The plates were incubated at 37°C for 8 to 17 h after which 3 to 5 ml of BSG was poured onto the plates with the filter inverted and subsequent resuspension of bacteria using a micropipette. The resuspended bacteria were serially diluted in BSG and 100 μ l samples of the 10^0 , 10^{-1} , and 10^{-2} dilutions were plated on selective media which was Luria agar containing 100 mg streptomycin/ml but lacking DAP (to select against growth of MGN-617). The plates were incubated at 37° C over night with the expectation of recovering some 30 colonies per plate from the 10^{-2} dilution and 200 colonies or so per plate for the 10^{-1} dilution. After overnight incubation, the plates were sprayed with a 250 mM catechol solution and yellow colonies which appeared within 5 min

were restreaked to obtain isolated colonies on Luria agar containing streptomycin. These colonies are merodiploids for the *asd* gene in that the suicide vector pMEG-223 with the $\Delta asdA20::xylE$ allele was inserted into the chromosome which still had the wild-type *asd* allele. Small cultures of individual colonies were prepared and plated on Luria agar containing 100 μ g DAP/ml plus 5% sucrose. Sucrose-resistant colonies, indicating recombinational loss of the suicide vector, were then sprayed with 250 mM catechol solution and yellow colonies picked, restreaked, and tested for DAP requirement by streaking on media with and without DAP. XylE expressing DAP-requiring colonies were also verified to be streptomycin sensitive and sucrose resistant, both indicating loss of genes present on the suicide vector pMEG-223. The extent of the deletion and the insertion were confirmed by PCR.

FIG. 6B specifies the nucleotide sequence of the $\Delta asdA20::xylE$ allele (SEQ ID NO:3) which includes 244 bp upstream of the *asd* ATG start site, an ORF containing the first 273 bp of the 5' portion of the *asd* gene, a 957 bp fragment containing the *xylE* gene which replaces a 729 bp deletion of the *asd* gene between the *EcoRV* sites, and is followed by a 174 bp region from the 3' portion of the *asd* ORF, and lastly the 315 bp downstream from the *asd* ORF.

3. Generation of Asd⁺ Vectors Possessing the *NcoI* Initiation Cloning site and Having Various Copy Numbers Specified by Different Plasmid Replicons.

The level of foreign proteins, especially antigens, expressed by recombinant bacteria having a Δasd mutation in the chromosome and an Asd⁺ vector is dependent upon the plasmid copy number when expression is driven by the constitutive promoter P_{trc}. For this reason, the Asd⁺ vector pYA292 (Figure 16 of U.S. Pat. 5,672,345) was modified in several ways.

In one modification the multiple cloning site (MCS) in FIG. 6 of U.S. Pat. 5,672,345 was modified to allow insertion of native full-length sequences commencing with the ATG start codon. This was accomplished by using PCR to delete two Cs following the ATG start codon in the MCS. This generated the *NcoI* recognition sequence CCATGG and changed the amino acid coding sequence in the MCS downstream from the *NcoI* site. This modified sequence (SEQ ID NO:8) is depicted in FIG. 7.

A second modification deleted the 750 base pair *HindIII* fragment encoding the *lacZ α* sequence present on pYA292 (Figure 16 of U.S. Pat. 5,672,345). Originally, the *lacZ α* sequence was used for detection of successful cloning by examining for the presence or absence of complementation as indicated by blue versus white colonies on agar medium with X-Gal. However, in many instances the *lacZ α* fragment coding sequence was tacked on to the

C-terminal end of other proteins, such that in-frame constructs would yield a blue reaction suggesting a failure when, in fact, successful cloning had been achieved. Also when the cloning event yielded out-of-frame constructs, the production of a C-terminal peptide sequence that was somewhat toxic often resulted. Since the cloning process was never a problem, the 750 base pair sequence in pYA292 was deleted to generate the plasmid pYA810.

In a third modification, a plasmid was constructed, pYA3332, which has the *NcoI* site and lacks the *lacZa* sequence but retains the p15A replicon, allowing about 20 plasmid copies per chromosome DNA equivalent. That plasmid is depicted in FIG. 8. The 830 base pair sequence between the *AccI* and *XbaI* site which contains the p15A origin of replication was replaced with the 1055 bp pBR origin of replication or the 884 bp pUC origin of replication to yield pYA3333 and pYA3334, respectively (FIG. 8). pYA3333 is present in 50 to 80 copies per chromosome DNA equivalent, whereas pYA3334 is present at 150 to 200 copies per chromosome DNA equivalent. When the same DNA sequence encoding a foreign gene product is inserted into the MCS in these three vectors and they in turn are electroporated into an *E. coli* or *S. typhimurium* Δasd mutant, the level of foreign protein synthesized is more or less proportional to the plasmid copy number with the highest level of protein expressed in the strain having the recombinant pYA3334 vector, the intermediate level produced by the strain possessing the pYA3333 vector, and the lowest level of protein produced in the strain with the pYA3332 vector.

4. Construction of Asd⁺ Vectors with Reduced Expression of the *asd* Gene.

Studies were performed to determine whether the recombinant Asd⁺ strains of the present invention exhibited wild-type virulence and were not attenuated due to overproduction of either plasmid DNA or, especially, the Asd enzyme. In this regard, the virulence of the *S. typhimurium* UK-1 strain MGN-023 with various plasmid vectors was evaluated. That strain possesses the $\Delta asdA16$ allele as the mutated essential gene, but is able to synthesize DAP when a plasmid vector comprising a complementing *asd* gene is present. Here, the complementing plasmids have differing copy numbers through utilization of different origins of replication.

Strains derived from MGN-023 were therefore constructed with plasmids containing an *asd* complementing recombinant gene along with (a) the pSC101 origin of replication (pYA3074), giving a very low level of Asd enzyme synthesis; (b) the p15A origin of replication (pYA292) giving a higher level of synthesis of the Asd enzyme; (c) the pBR322 origin of replication (pYA3149), yielding a still higher level of Asd enzyme synthesis; and (d) the pUC origin of replication (pYA3137), giving the highest level of Asd enzyme synthesis.

Mice were inoculated with various amounts of the recombinant bacteria as previously described, and the virulence of the bacteria was determined and an LD₅₀ for the various bacteria was calculated. Results of these experiments are shown in Table 3. MGN-023 with pYA3137, having the pUC origin of replication, was significantly less virulent than any of the recombinant strains of the wild-type *S. typhimurium* UK-1 parent, χ 3761. Replication studies with these strains generally found that the Asd⁺ vectors with the pBR origin of replication were slightly attenuated and that Asd⁺ vectors with a pUC origin were more significantly attenuated, suggesting that overproduction of the Asd enzyme is attenuating.

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TABLE 3

Mortality of 8-week-old BALB/c mice 30 days after oral inoculation with *S. typhimurium* UK-1 strain MGN-023 ($\Delta asdA16$) containing Asd⁺ vectors with different copy numbers.

Strain	Genotype	Inoculating dose (DFU)	Survivors/ total	MMD*	LD ₅₀ (CFU)
χ3761	wild-type	1.54 x 10 ⁶	1/4	11.6	7.1 x 10 ⁴
		1.54 x 10 ⁵	1/4	10.6	
		1.54 x 10 ⁴	3/4	10.0	
		1.54 x 10 ³	4/4		
			(9/16)		
MGN-023 pYA3074	Δ <i>asdA16</i> containing Asd ⁺ vector with pSC101 origin	1.70 x 10 ⁶	0/4	12.7	4.0 x 10 ⁵
		1.70 x 10 ⁵	4/4		
		1.70 x 10 ⁴	3/4	13.0	
		1.70 x 10 ³	4/4		
			(11/16)		
MGN-023 pYA292	Δ <i>asdA16</i> containing Asd ⁺ vector with p15A origin	1.42 x 10 ⁶	2/4	10	3.3 x 10 ⁵
		1.42 x 10 ⁵	3/4	16	
		1.42 x 10 ⁴	3/4	20	
		1.42 x 10 ³	3/4	23	
			(11/16)		
MGN-023 pYA3149	Δ <i>asdA16</i> containing Asd ⁺ vector with pBR322 origin	1.34 x 10 ⁶	1/4	12	2.2 x 10 ⁴
		1.34 x 10 ⁵	0/4	15.7	
		1.34 x 10 ⁴	2/4	16.5	
		1.34 x 10 ³	4/4		
			(7/16)		
MGN-023 pYA3137	Δ <i>asdA16</i> containing Asd ⁺ vector with pUC origin	1.54 x 10 ⁶	4/4		>1.54 x 10 ⁶
		1.54 x 10 ⁵	4/4		
		1.54 x 10 ⁴	4/4		
		1.54 x 10 ³	4/4		
			(16/16)		

*MDD: Mean no. days to death

Based on previous results, it is apparent that the use of pBR- and pUC-based Asd⁺ vectors to induce high-level immune responses to an expressed foreign antigen might be compromised by overproduction of the Asd enzyme. Therefore, experiments were conducted to determine whether the *asd* coding sequence could be truncated to reduce its level of expression.

The *asd* gene sequence was amplified by PCR starting at base pair 286 and ending on base pair 1421 (see FIG. 2A). This sequence contains the Shine-Dalgarno (SD) sequence for ribosome recognition but lacks the RNA polymerase -35 recognition sequence and the promoter -10 sequence and ends just after the *asd* gene TAG stop codon with an additional terminal T. This PCR fragment was synthesized with an N-terminal *Bgl*III site and a C-terminal *Xba*I site. After cleavage with *Bgl*III and *Xba*I, the sequence was used to construct various Asd⁺ vectors such as pYA3342 (pBR ori) and pYA3341 (pUC ori) (FIG. 9). After religation, the recombinant vectors were electroporated into Δ *asd* *E. coli* strain χ 6212 to select DAP-independent recombinants. The plasmids were then reisolated from these recombinants and introduced into the Δ *asdA16* *S. typhimurium* strain MGN-023 for selection of DAP-independent recombinants. Surprisingly, DAP-independent clones were obtained. Therefore, the *asd* gene with its SD sequence but lacking the -35 and -10 components of its promoter is transcribed to yield enough *asd* mRNA to permit synthesis of enough Asd enzyme and DAP to retain cell viability.

In comparing *E. coli* and *S. typhimurium* strains with the plasmid vectors pYA3333 and pYA3334 (FIG. 8) and strains with plasmids pYA3342 and pYA3341 (FIG. 9), it appeared that strains with the latter two plasmids grew more rapidly than those with the plasmid vectors specifying a higher level of Asd enzyme. This growth advantage effect was relatively minor, however, and it became of interest to see whether there was any difference in the genetic stability of strains. A procedure analogous to that described in Example 15 of U.S. Pat. 5,672,345 was therefore carried out. In this study, recombinant cultures were inoculated into 5 ml of Luria broth and incubated at 37° C overnight. The next morning the cultures were diluted 1:1000 into 5 ml of prewarmed Luria broth and the procedure repeated daily for at least five days. Since each 1:1000 dilution constitutes ten generations of growth, a total of 50 or 60 generations of growth were permitted for cells grown either in the presence or absence of DAP. For all strains with all Asd⁺ plasmids 100% of over 100 colonies tested for each strain after 10, 20, 30, 40, and 50 generations of growth remained Asd⁺ and contained plasmid DNA.

Another important parameter to evaluate is whether the amount of Asd enzyme was significantly reduced in strains possessing pYA3342 and pYA3341 compared to strains with plasmids pYA3333 and pYA3334 that had *asd* genes with the *asd* promoter. FIG. 10 presents the results of an experiment in which strains were grown in Luria broth and a constant amount of protein was loaded on a polyacrylamide gel and electrophoresed after which a Coomassie brilliant blue stain was used to identify protein bands. As is readily seen, protein bands having the size of the Asd protein (39kDa) are readily apparent in bacteria having Asd⁺ plasmids with the *asd* promoter and are not readily detectable in protein extracts from cells harboring the pYA3342 and pYA3341 plasmids with the SD-*asd* sequence lacking the *asd* promoter. These results thus explain the better growth of strains having the plasmids with the SD-*asd* sequence and also warrants their use in vaccine compositions since there would be less competition for the protein synthesis machinery and more could be devoted to synthesizing a foreign protein, especially an antigen, encoded by a sequence cloned into the Asd⁺ vector multiple cloning site. It should be apparent from these considerations that decreasing the level of Asd protein synthesis also reduces the selective pressure against maintenance of the plasmid and thus should enhance the utility of strains harboring these plasmid vectors for any of their intended uses. In this regard, *S. typhimurium* UK-1 MGN-023 with the Δ *asdA16* mutation could be restored to wild-type virulence by introducing either pYA3342 or pYA3341, results that justify the advantage of reducing the level of Asd enzyme synthesized by strains with Asd⁺ vectors.

Although *E. coli* and *S. typhimurium* strains with a Δ *asd* mutation and possessing the plasmids pYA3342 or pYA3341, each with the SD-*asd* sequence, grow at the same rate in medium with or without DAP, it is apparent that such cells transcribe, by some unknown mechanism, a sufficient amount of mRNA to cause synthesis of a sufficient amount of Asd protein to carry out the biosynthetic pathway to synthesize DAP. That is, they synthesize enough DAP so that DAP is not limiting for growth. However, numerous attempts to subclone the *Bgl*III-*Xba*I fragment containing the SD-*asd* sequence into plasmid vectors with either the p15A replicon or the pSC101 replicon, which has an even lower copy number than the p15A replicon, were unsuccessful. It is therefore apparent that in these cases there is an insufficient number of copies of the plasmid DNA so that chance transcription would synthesize a sufficient amount of mRNA to cause synthesis of enough Asd enzyme to support growth in the absence of exogenously supplied DAP. This hypothesis was confirmed by the ability to make such constructs and introduce them into cells provided that DAP was contained in the medium. In all cases, removal of DAP from the growth medium led to the inability of the recombinant cells to grow and survive.

As would be understood by the skilled artisan, the above-described scheme of retaining the SD sequence but eliminating the -35 polymerase recognition sequence and the promoter -10 sequence would also be useful for other selective markers when a high copy number plasmid is used, for example when high levels of expression of a desired gene is useful, but where the concurrent excessive expression of the selective marker is disadvantageous. Non-limiting examples of other selective markers useful in these embodiments are drug resistance markers, *purA*⁺, *purB*⁺, *thyA*⁺, and *trp*⁺.

5. Complementation and Possibilities of Recombination Between *Asd*⁺ Vectors and Chromosome with Δ *asd* Mutations.

With transposon-induced Δ *asd* mutations, much or all of the *asd* gene was deleted, but importantly also DNA sequences flanking the *asd* gene such that it was always impossible to have a double crossover event between the wild-type *asd* sequence on any of the *Asd*⁺ plasmid vectors constructed and the chromosome to result in restoration of the chromosome to an *asd*⁺ genotype. This is because one of the recombination events must be on one side of the chromosomal deletion mutation encompassing the *asd* gene and the other must be on the other side of this deletion mutation. As depicted in FIG. 11, the Δ *asdA16* chromosomal mutation deletes bp 219 to 1460 inclusive of the DNA sequence encoding *asd* and its 5' and 3' flanking regions (FIG. 2A). The pYA3332, pYA3333, and pYA3334 *Asd*⁺ vectors have the entire 1735 base pair sequence, thus having 218 bp of homology 5' to the Δ *asdA16* mutation and 275 bp 3' to the Δ *asdA16* deletion. Thus, it is possible that double homologous recombination events could occur to enable the *Asd*⁺ sequence present in these *Asd*⁺ vectors to recombine with the chromosome to eliminate the Δ *asdA16* mutation and replace it with the vector wild-type *Asd*⁺ sequence. In contrast, the plasmids pYA3342 and pYA3341 only contain the SD-*asd* sequence going from 286 bp to 1421 bp (FIG. 2A) and there is no nucleotide sequence homology remaining in those vectors with the chromosome remaining in strains that have the Δ *asdA16* mutation. This is readily seen by examination of the top portion of FIG. 11. Although we have seen complete stability in maintenance of *Asd*⁺ plasmids with or without recombinant foreign gene inserts encoding proteins, especially antigens, in strains possessing the Δ *asdA16* mutation, it is desirable to determine whether the balanced-lethal host-vector systems comprising nucleotide sequence homology between sequences on the vector and sequences in the chromosome (enabling double crossover events to occur) did in fact impair the utility of the balanced-lethal host-vector systems. In order to evaluate this, it was critically important to be able to recognize with a high degree of precision and with ability to detect very rare events the potential loss of the Δ *asd* mutation in

the chromosome. For this reason, the $\Delta asdA20::xylE$ construction was made since cells harboring this deletion mutation with or without an Asd^+ plasmid become yellow following spray with catechol. As can be seen in the bottom portion of Figure 11, plasmids such as pYA3332, pYA3333, and pYA3334 possess regions of DNA sequence homology, both 5' and 3' to the internal deletion of 729 bp of the *asd* gene and the *xylE* coding sequence. Thus the plasmids pYA3332, pYA3333, and pYA3334 possess 517 bp of homology 5' to the deletion and 499 bp 3' to the deletion. In these cases the lengths of homologous sequences are longer than when these same Asd^+ plasmids are present in bacterial strains with the $\Delta asdA16$ mutation. Also, there is homology between the SD-*asd* sequence on pYA3342 and pYA3341 and sequences 5' and 3' to the $\Delta asdA20::xylE$ mutation in the chromosome. In this case, there is 232 bp 5' to the deletion and 175 bp 3' to the deletion, thus making double crossover recombination theoretically possible so as to replace the chromosomal $\Delta asdA20::xylE$ mutant allele with the wild-type SD-*asd*⁺ sequence on the Asd^+ plasmids.

To evaluate the stability of plasmid constructs in *Salmonella* strains with defined deletions of the *asd* gene we explored the stability after repetitive growth cycles in the presence of DAP in vitro and then investigated for stability after immunization of female BALB/c mice with recombinant constructs. For the in vitro evaluations, we therefore constructed recombinants by introducing the pBR based replicon pYA3342 possessing the SD-*asd* sequence into $\chi 8315$ ($\Delta phoPQ23 \Delta asdA20::xylE$) and into $\chi 8316$ ($\Delta poxA270 \Delta asdA20::xylE$). Overnight cultures in Luria broth of the recombinant constructs were diluted 1:1000 (5 μ l into 5 ml) in prewarmed Luria broth containing 50 μ g DAP /ml and grown without aeration at 37° C for 16 h. The next day the cultures were diluted and plated on L agar plus DAP and incubated at 37° C. One hundred colonies of each of the strains were picked and inoculated onto L agar with or without DAP to determine loss of the vector. Colonies grown on L agar without DAP were considered Asd^+ . After incubation, colonies were sprayed with 250 mM catechol to determine loss of the *xylE* marker. Yellow colonies were considered $XylE^+$. The process was repeated daily for five days until the culture had grown to the 50th generation. The results are presented in Table 4, and indicate that all 100 colonies from both strains after 10, 20, 30, 40, and 50 generations of growth were phenotypically Asd^+ and $XylE^+$. In addition, six colonies of each strain were picked and grown up with DAP and the presence of the plasmid was examined; all 30 isolates of both strains contained pYA3342. Thus even though double crossover recombination between the sequence in pYA3342 and the sequences flanking the *xylE* insert in the $\Delta asdA20::xylE$ mutation were possible, no such recombinations occurred at detectable frequencies.

Table 4

In vitro stability of *xylE* marker in χ 8315 (Δ *phoPQ23* Δ *asdA20::xylE*)(pYA3342) and χ 8316 (Δ *poxA270* Δ *asdA20::xylE*)(pYA3342) in Luria broth plus DAP

5	Strains	Number of Asd ⁺ XylE ⁺ colonies/100 colonies tested*				
		10 Gen	20 Gen	30 Gen	40 Gen	50 Gen
	χ 8315(pYA3342)	100	100	100	100	100
	χ 8316(pYA3342)	100	100	100	100	100

10

*No Asd⁺ XylE⁺ colonies were observed.

A more permissive test was conducted by introducing the pBR based plasmid pYA3333 into χ 8315 and χ 8316 since the regions of DNA sequence homology to enable double crossover events is more extensive (see FIG. 11, bottom). The experiment to evaluate in vitro stability was repeated exactly as had been done for the strains possessing pYA3342. In this case, all 100 colonies from both strains after 10, 20, 30, 40 and 50 generations of growth were phenotypically Asd⁺ and XylE⁺ and of the 6 colonies of each strain evaluated after each growth cycle all possessed the plasmid pYA3333. Thus even though double crossover recombination is more likely in these constructs because of the more substantial amount of DNA sequence homology flanking the *xylE* insertion into the Δ *asdA20* allele in the chromosome, no such double crossover events were detected.

Even greater selective pressure was applied by introducing recombinant strains by oral inoculation into mice and evaluating recovered microorganisms for the relevant phenotypes. For these experiments the bacterial strains were grown over night in static cultures in Luria broth. The next day, cultures were diluted 1:100 into prewarmed Luria broth and grown with aeration by shaking until an OD 600 of 0.85 was reached. The cultures were sedimented by centrifugation at room temperature using the SS3A rotor at 6500 rpm for 20 min. Bacterial cells were resuspended in BSG to a proper concentration and titration by dilution was performed to assess the CFUs/ml in the concentrated suspensions. Eight week old female BALB/c mice that had been acclimated in our animal facility for one week prior to use were inoculated orally with 20 μ l containing 10⁹ CFU of the bacterial strain. Five mice were used for each of the four strains evaluated. Peyer's patches and spleens of all mice were taken at seven and ten days after oral inoculation. Tissues were homogenized and plated on MacConkey agar containing 1% lactose and 50 μ g DAP/ml. One hundred colonies from each

vector. In the experiment with χ 8315 and χ 8316 possessing the *asd* vector pYA3333 we observed total stability in bacteria recovered seven days after oral inoculation, with all bacteria being Asd⁺ and XylE⁺ and all tested isolates still possessed the Asd⁺ plasmid pYA3333 (Table 6). On the other hand, 8 of 93 isolates obtained 10 days following oral inoculation of mice with χ 8315 containing pYA3333 had lost the chromosomal *asd* mutation with the *xylE* insertion but remained Asd⁺ because of replacement of the chromosomal mutant allele by double crossover recombination. No such isolates were observed 10 days after oral inoculation with the Δ *poxA270* strain χ 8316 (Table 6).

Table 5

In vivo stability of *xylE* marker in χ 8315 (Δ *phoPQ23* Δ *asdA20::xylE*) (pYA3342) and χ 8316 (Δ *poxA270* Δ *asdA20::xylE*)(pYA3342) in mice*.

5

Strains	Asd ⁺	Asd ⁺ XylE ⁺	Asd ⁺ XylE ⁻
χ 8315(pYA3342)	200/200	200/200	0/200
χ 8316(pYA3342)	200/200	200/200	0/200

- 10 * Bacteria were isolated from internal lymphoid organs of mice on day 10 after oral inoculation with 10⁹ CFU and plated on MacConkey agar + Lactose + DAP and replica plated onto L agar with or without DAP and then sprayed with 250 mM catechol solution.

15

Table 6

Frequency of loss of Asd⁺ vector and/or *xylE* marker in χ 8315 (Δ *phoPQ23* Δ *asdA20::xylE*)(pYA3333) and χ 8316 (Δ *poxA270* Δ *asdA20::xylE*)(pYA3333) in mice*.

	Days	Strains	Asd ⁺	Asd ⁺ XylE ⁺	Asd ⁺ XylE ⁻
20	7	χ 8315(pYA3333)	100/100	100/100	0/100
	10	χ 8315(pYA3333)	93/93	85/93	8/93
	7	χ 8316(pYA3333)	100/100	100/100	0/100
	10	χ 8316(pYA3333)	100/100	100/100	0/100

- 25 * Bacteria were isolated from internal lymphoid organs of mice on days 7 and 10 after oral inoculation and plated on MacConkey agar + Lactose + DAP and replica plated onto L agar with or without DAP and then sprayed with 250 mM catechol solution.

30 Taken collectively, the experiments of recovering microorganisms following oral inoculation of mice revealed that the theoretical possibility of recombination can occur with very low frequency after numerous generations of growth under highly selective in vivo conditions, at least in one of the two instances studied.

35 It is apparent from these results that the theoretical possibility of recombination does not mandate that such recombination does indeed occur or occurs at frequencies that would compromise the use of these balanced-lethal host-vector systems. In this regard, it should be

recalled that use of recombinant attenuated *S. typhimurium* vaccine strains that had plasmid vectors encoding a foreign antigen and which were maintained in vitro by growth in the presence of antibiotics to which the plasmid vector conferred resistance, often led to no more than 10 percent of the *Salmonella* cells recovered as soon as three days after oral inoculation of mice retaining the plasmid vector and expressing the foreign antigen (see Nakayama et al., 1988; Curtiss et al., Curr. Top. Microbiol. Immun. 146:35-49, 1989).

There are several possible explanations for the functional stability of the recombinant strains described in this Example. First, transient integration of the plasmid into the chromosome, even if followed soon thereafter by a second recombination event excising the plasmid from the chromosome, may be inhibited when there are multiple copies of plasmid DNA in the cytoplasm of the bacterial cells. It is well known that plasmids capable of integration do so and then generally preclude the maintenance of plasmids in the cytoplasm and similarly, plasmids existing in the cytoplasm seem to interfere with the common presence of the plasmid sequence in the chromosome. This is best understood from studies in the 1950s and 1960s on the inability of the F plasmid to be stably maintained in Hfr cells that possess the same F plasmid integrated into their chromosome. In F^+ cells with F in the cytoplasm, rare F integration events occur in which F replicates under control of chromosome replication with the consequence that the cytoplasmic F disappears. Similarly, it is well known that λ lysogens with λ prophage integrated into the chromosome fail to support lambda replication in the cytoplasm. Thus, co-existence of cytoplasmic and integrated states of Asd^+ vectors, even though transient, may be inhibited from occurrence. A second factor possibly contributing to the rarity of a double crossover event which would be necessary for allele exchange with the wild-type plasmid *asd⁺* allele replacing the chromosomal mutation is the phenomenon of positive interference, well known in the genetics of *Drosophila* and maize but also studied and recognized to occur in bacteria such as *E. coli* (Curtiss, J. Bacteriol. 89:28-40, 1965). In this case, the deletion of sequences in the chromosome necessitates that the wild-type sequence has to undergo a convolution to allow for effective homologous pairing between regions of homology on either side of the deleted sequence in the chromosome. Such effective homologous pairing is an essential first step preparatory to the recombination event. Such contortions reduce the likelihood of a second recombination event following a first event, so-called positive interference. It is also possible, of course, that the introduction of the *xylE* marker which is totally non-homologous to any sequence in the Asd^+ vectors, also serves to cause positive interference and reduce the likelihood of double crossover events even though DNA sequence homology exists. Whatever the explanation, it is clear that the existence of some DNA sequence homology on either side of a deletion in the chromosome

with sequences on the Asd⁺ vector does not interfere with the functional integrity of the balanced-lethal host-vector system over a number of generations either in vitro or following inoculation into an animal. The recombinant constructs illustrated in these Examples which possess such DNA sequence homologies can more than adequately perform the tasks that they are designed to do whether it be to immunize an animal host against an expressed foreign antigen or to produce a protein that has some other biological beneficial attribute.

6. DNA Vaccines Produced and/or Delivered by Bacteria Comprising a Functional Balanced-Lethal Host-Vector System.

DNA vaccines for immunization of individuals by direct inoculation of plasmid DNA molecules encoding the antigens from viruses, parasites, bacteria, or fungi for synthesis within and by the immunized eukaryotic host is receiving significant attention with some very encouraging results from numerous studies. See, e.g., Ulmer et al (1996a); Ulmer et al (1996b); Whalen (1996); Robinson (1997). Most of the DNA vaccine vectors possess either a kanamycin-resistance determinant or an ampicillin-resistance gene to enable maintenance of the plasmid constructs in *E. coli* strains by growth in the presence of kanamycin or ampicillin. As stated above, the addition of kanamycin or ampicillin is an expense during fermentation to produce quantities of DNA vaccine vector to use for immunization. In addition kanamycin or ampicillin must be completely removed prior to use of the DNA plasmids for immunization. Lastly, there is concern about the introduction of antibiotic resistant genes into individuals whether stably inheriting that genetic information or not. It is also known that the presence of CpG sequences that remain unmethylated in bacterial DNA when introduced into eukaryotic cells, especially antigen processing and presenting cells such as macrophages, augment the immune response to expressed foreign antigens in a significant way (see, e.g., Krieg et al., 1998, for a review). Unfortunately, the DNA sequence encoding kanamycin resistance lacks the types of CpG sequences that maximize the enhancement of the immune response. On the other hand, the *asd*⁺ gene of *S. typhimurium* possesses two such sequences. It is therefore possible to construct derivatives of eukaryotic DNA vaccine vectors such as pVAX-1 by substituting the kanamycin resistance gene with the *S. typhimurium asd* gene. If a high copy number pUC vector is used, the *asd* sequence can be the SD-*asd* sequence lacking the promoter so that the amount of Asd enzyme is diminished to a level necessary to support growth and constitute a balanced-lethal host-vector system but not to result in any selective pressure that would lead to a lower plasmid copy number or poor growth properties of the recombinant constructs. Such a pVAX *asd* vector is diagrammed in FIG. 12. Such a vector can also be directly delivered by an attenuated bacterial DNA vaccine delivery host to

immunize vertebrates against antigens specified by plasmid encoded genes. In these plasmids, expression of the antigen is controlled by (i.e., operably linked to) a eukaryotic promoter. A preferred promoter for this purpose is an immediate-early promoter from a cytomegalovirus ("a CMV promoter"), as in the vector depicted in FIG. 12. For reviews of bacterial delivery of DNA vaccines, see, e.g., Detrich et al. (1999); Detrich et al. (2000).

7. Use of nucleotide sequence information for *dapA*, *dapB*, *dapD*, *dapE*, and *dapF* genes to construct and evaluate functional balanced-lethal host-vector systems.

The nucleotide sequences for the *dapA*, *dapB*, *dapD*, *dapE* and *dapF* genes of *E. coli* and *S. typhimurium* are now known. See Table 7. This information can be used to generate defined deletion mutations and introduce them into the chromosome, as described in Example 1 for the *asd* gene, to construct defined deletion mutations with a reporter gene such as *xylE* as described in Example 2, to insert these into plasmid vectors with suitable multiple cloning sites and absence of extraneous coding sequences as illustrated in Example 3, to diminish the level of expression of the DapA, DapB, DapD, DapE or DapF enzymes to an amount necessary for growth in the absence of DAP but without constituting an energy burden on cells as described in Example 4, to evaluate the functional utility and stability in vitro and in vivo of these balanced-lethal host-vector constructs as described in Example 5, and to generate DNA vaccine vectors possessing the *dapA*, *dapB*, *dapD*, *dapE*, or *dapF* sequences as described for the *asd* gene in Example 6. Other manipulations described herein for *asd* could also be adapted by the skilled artisan to the use of the *dapA*, *dapB*, *dapD*, *dapE*, or *dapF* sequences.

Table 7

Genbank sequences encoding DapA, DapB, DapD, DapE and DapF.

	<i>Salmonella typhimurium</i> (Washington University)		<i>Salmonella typhi</i>	
	Contig.	Corresponding segment	Contig.	Corresponding segment
<i>dapA</i> (Dihydrodipicolinate synthetase)	295	786-1295	9	82379-83254
<i>dapB</i> (Dihydrodipicolinate reductase)	1123	8-505	1693	14904-15722
<i>dapD</i> (Succinyl-diaminopimelate aminotransferase)	3548	1-78	1693	188012-187191
<i>dapE</i> (N-succinyl-diaminopimelate)	50	228-515	9	89605-88481
<i>dapF</i> (Diaminopimelate epimerase)	436	47869-47045	1694	43662-42838

Industrial Applicability

- 5 The present invention discloses microbial cells that have an inactivating mutation in a native essential gene encoding an essential enzyme that catalyzes a step in the biosynthesis of DAP. The cells also comprise extrachromosomal vectors comprising (a) a recombinant gene which complements the inactivated native essential gene, and (b) a desired gene, encoding a desired gene product. These cells are particularly useful in (1) methods for immunization of a
- 10 vertebrate, where the microbial cells are live vaccine components, and where the desired gene encodes an antigen to which immunity is induced, or an allergen to which the vertebrate is to be desensitized, or sperm-specific and egg-specific autoantigens to arrest fertility, or specific antibodies, e.g., which bind to tumors or pathogens such as viruses, fungi, parasites, or bacteria, or gene products essential for a pathogen to cause disease), or enzymes that have the
- 15 potential to convert prodrugs into toxic drugs within a tumor cell mass in an individual with a solid tumor; and (2) methods for delivering a desired gene product to a vertebrate, where the desired gene encodes, for example an immunomodulatory therapeutic desired gene product such as a lymphokine or cytokine; and other purposes which would be known to the skilled artisan. Methods are also provided for producing improved DNA vaccines.
- 20 All references cited in this specification are hereby incorporated in their entirety by reference. The discussion of the references herein is intended merely to summarize the assertions made by their authors and no admission is made that any reference constitutes prior art. Applicant reserves the right to challenge the accuracy and pertinence of the cited references.

I claim:

1. An attenuated derivative of a pathogenic microorganism with a cell wall comprising diaminopimelic acid (DAP) which further comprises:
 - (a) an inactivating mutation in a native chromosomal essential gene encoding an essential enzyme which catalyzes a step in the biosynthesis of DAP;
 - (b) a recombinant complementing gene on an extrachromosomal vector encoding a functional replacement for the essential enzyme, wherein the complementing gene can recombine to replace the defective chromosomal gene; and
 - (c) a desired gene on the extrachromosomal vector, wherein the desired gene is a recombinant gene encoding a desired gene product;
 wherein the desired gene is stably maintained in a progeny population of the microorganism.
2. The microorganism of claim 1, wherein the microorganism is a member of the *Enterobacteriaceae* and the extrachromosomal vector is a plasmid.
3. The microorganism of claim 2, further comprising an inactivating mutation in a native gene selected from the group consisting of a *pab* gene, a *pur* gene, an *aro* gene, *nadA*, *pncB*, *galE*, *pmi*, *fur*, *rpsL*, *ompR*, *htrA*, *hemA*, *cdt*, *cya*, *crp*, *dam*, *phoP*, *phoQ*, *rfc*, *poxA*, *galU*, *mviA*, *sodC*, *recA*, *ssrA*, *sirA*, *inv*, *hilA*, *rpoE*, *flgM*, *tonB*, and *slyA*.
4. The microorganism of claim 3, wherein the desired gene product is an antigen.
5. The microorganism of claim 4, wherein the antigen is selected from the group consisting of a bacterial antigen, a viral antigen, a fungal antigen, a parasitic antigen, a gamete-specific antigen, an allergen, and a tumor antigen.
6. The microorganism of claim 2, wherein the essential gene is selected from the group consisting of *dapA*, *dapB*, *dapD*, *dapE*, *dapF*, and *asd*.
7. The microorganism of claim 6, wherein the inactivating mutation is in an *asd* gene and comprises an insertion or a deletion.

8. The microorganism of claim 2, wherein the recombinant complementing gene lacks an RNA polymerase -35 recognition sequence and a promoter -10 sequence.

9. The microorganism of claim 8, wherein the recombinant complementing gene is an *asd* gene.

10. The microorganism of claim 2, wherein the desired gene is operably linked to a eukaryotic promoter.

11. The microorganism of claim 10, wherein the eukaryotic promoter is a CMV promoter.

12. A recombinant vector comprising a recombinant gene encoding an essential enzyme, wherein the recombinant gene lacks an RNA polymerase -35 recognition sequence and a promoter -10 sequence,

5 wherein the vector can functionally replace the essential enzyme when the vector is present in a microorganism having an inactivating mutation in a native gene encoding the essential enzyme.

13. The recombinant vector of claim 12, wherein the vector is a plasmid capable of expressing the essential enzyme in a microorganism that is a member of the *Enterobacteriaceae*.

14. The recombinant vector of claim 12, wherein the essential enzyme catalyzes a step in the biosynthesis of DAP.

15. The recombinant vector of claim 14, wherein the recombinant gene is an *asd* gene.

16. The recombinant vector of claim 12, further encoding a desired gene product.

17. The recombinant vector of claim 16, wherein the desired gene product is an antigen.

18. The recombinant vector of claim 17, wherein the antigen is selected from the group consisting of a bacterial antigen, a viral antigen, a fungal antigen, a parasitic antigen, a gamete-specific antigen, an allergen, and a tumor antigen.

19. The recombinant vector of claim 16, wherein the desired gene product is therapeutic to a vertebrate.

20. The recombinant vector of claim 19, wherein the desired gene product is selected from the group consisting of a lymphokine, a cytokine, and a sperm-specific or egg-specific autoantigen.

21. The recombinant vector of claim 16, wherein the desired gene product is operably linked to a eukaryotic promoter.

22. The recombinant vector of claim 21, wherein the eukaryotic promoter is a CMV promoter.

23. A method of selecting for the presence of a desired gene in a population of microbial cells having an inactivating mutation in a native chromosomal gene encoding an essential enzyme which catalyzes a step in the biosynthesis of DAP, the method comprising

- 5 (a) transfecting the microbial cell with an extrachromosomal vector having
 - (i) the desired gene, and
 - (ii) a recombinant complementing gene encoding a functional replacement for the essential enzyme, wherein the complementing gene can recombine to replace the defective chromosomal gene; then
- 10 (b) culturing the microbial cell.

24. The method of claim 23, wherein the microbial cell is a member of the *Enterobacteriaceae*.

25. The method of claim 24, wherein the microbial cell further comprises an inactivating mutation in a native gene selected from the group consisting of *aroA*, *aroC*, *aroD*, *cdt*, *cya*, *crp*, *phoP*, *phoQ*, *ompR*, *galE*, and *htrA*.

26. The method of claim 24, wherein the desired gene product is an antigen.

27. The method of claim 26, wherein the antigen is selected from the group consisting of a bacterial antigen, a viral antigen, a fungal antigen, a parasitic antigen, a gamete-specific antigen, an allergen, and a tumor antigen.

28. The method of claim 23, wherein the desired gene product is selected from the group consisting of a lymphokine, a cytokine, and a sperm-specific or egg-specific autoantigen.

29. The method of claim 23, wherein the desired gene is operably linked to a eukaryotic promoter.

30. A vaccine for immunization of a vertebrate, the vaccine comprising live bacterial cells of an attenuated derivative of a pathogenic bacterium in a pharmaceutical carrier, the bacterial cells comprising:

- 5 (a) an inactivating mutation in a native chromosomal essential gene encoding an essential enzyme which catalyzes a step in the biosynthesis of DAP;
 - (b) a recombinant complementing gene on an extrachromosomal vector encoding a functional replacement for the essential enzyme, wherein the complementing gene can recombine to replace the defective chromosomal gene; and
 - 10 (c) a desired gene on the extrachromosomal vector, wherein the desired gene is a recombinant gene encoding a desired gene product;
- wherein the desired gene is stably maintained in a progeny population of the microorganism.

31. The vaccine of claim 30, wherein the inactivating mutation is in an *asd* gene and comprises a deletion or an insertion.

32. The vaccine of claim 30, wherein the bacterium further comprises an inactivating mutation in a native gene selected from the group consisting of *aroA*, *aroC*, *aroD*, *cdt*, *cya*, *crp*, *phoP*, *phoQ*, *ompR*, *galE*, and *htrA*.

33. The vaccine of claim 30, wherein the desired gene product is an antigen.

34. The vaccine of claim 33, wherein the antigen is selected from the group consisting of a bacterial antigen, a viral antigen, a fungal antigen, a parasitic antigen, a gamete-specific antigen, an allergen, and a tumor antigen.

35. The vaccine of claim 30, wherein the recombinant complementing gene on an extrachromosomal vector lacks an RNA polymerase -35 recognition sequence and a promoter -10 sequence.

36. The vaccine of claim 30, wherein the desired gene is operably linked to a eukaryotic promoter.

37. A method of inducing immunoprotection in a vertebrate, comprising administering to the vertebrate the vaccine of claim 30.

38. A method of delivering a desired gene product to a vertebrate, the method comprising administering to the vertebrate live bacterial cells of an attenuated derivative of a pathogenic bacterium, the bacterial cells comprising:

- 5 (a) an inactivating mutation in a native chromosomal essential gene encoding an essential enzyme which catalyzes a step in the biosynthesis of DAP;
 - (b) a recombinant complementing gene on an extrachromosomal vector encoding a functional replacement for the essential enzyme, wherein the complementing gene can recombine to replace the defective chromosomal gene; and
 - 10 (c) a desired gene on the extrachromosomal vector, wherein the desired gene is a recombinant gene encoding the desired gene product;
- wherein the desired gene is stably maintained in a progeny population of the microorganism.

39. The method of claim 38, wherein the bacterium is an *Enterobacteriaceae* and the bacterium further comprises an inactivating mutation in a native gene selected from the group consisting of *aroA*, *aroC*, *aroD*, *cdt*, *cya*, *crp*, *phoP*, *phoQ*, *ompR*, *galE*, and *htrA*.

40. The method of claim 38, wherein the essential gene is selected from the group consisting of *dapA*, *dapB*, *dapD*, *dapE*, *dapF*, and *asd*.

41. The method of claim 38, wherein the desired gene product is an antigen.

42. The method of claim 38, wherein the desired gene product is therapeutic to the vertebrate.

-
- | Variable | Category | Percentage |
|----------------------------------|-------------------|------------|
| Age | 18-24 | 15% |
| | 25-34 | 25% |
| | 35-44 | 30% |
| | 45-54 | 20% |
| | 55-64 | 10% |
| Sex | Male | 60% |
| | Female | 40% |
| Education | High School | 30% |
| | College | 45% |
| | Graduate School | 25% |
| Income | \$10,000-\$19,999 | 15% |
| | \$20,000-\$29,999 | 25% |
| | \$30,000-\$39,999 | 30% |
| | \$40,000-\$49,999 | 20% |
| | \$50,000-\$59,999 | 10% |
| Marital Status | Single | 30% |
| | Married | 50% |
| | Divorced | 10% |
| | Widowed | 10% |
| Religion | Christianity | 60% |
| | Islam | 20% |
| | Hinduism | 10% |
| | Buddhism | 5% |
| | Other | 5% |
| Ethnicity | White | 60% |
| | Black | 20% |
| | Asian | 10% |
| | Hispanic | 5% |
| | Other | 5% |
| Political Affiliation | Democrat | 60% |
| | Republican | 30% |
| | Independent | 10% |
| Party Affiliation | Democratic Party | 40% |
| | Republican Party | 30% |
| | Green Party | 5% |
| | Libertarian Party | 5% |
| | Other | 20% |
| Ideology | Liberal | 40% |
| | Conservative | 30% |
| | Moderate | 20% |
| | Other | 10% |
| Attitude towards the environment | Strongly Oppose | 10% |
| | Oppose | 20% |
| | Neutral | 30% |
| | Support | 20% |
| | Strongly Support | 20% |
| Attitude towards the government | Strongly Oppose | 10% |
| | Oppose | 20% |
| | Neutral | 30% |
| | Support | 20% |
| | Strongly Support | 20% |

Abstract

10 DNA vaccines.

FIG. 2

A

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1  ggatcttccc taaattttaa tataaacaac gaattatctc cttaacgtac gttttcgttc
61  cattggccct caaaccctta attaggatca ataaaacagc gacggaaatg attcccttcc
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1501 aatttgtgtt aaaccagggg tgcacgtca ccctttttt gcgtaataca ggagtaaagc
1561 cagatgtttc atttttatca ggagttaagc agagcattgg ctattcttta agggtagctt
1621 aatcccacgg gtattaagcc taacctgaag gtaggacgac gcagatagga tgcacagtgt
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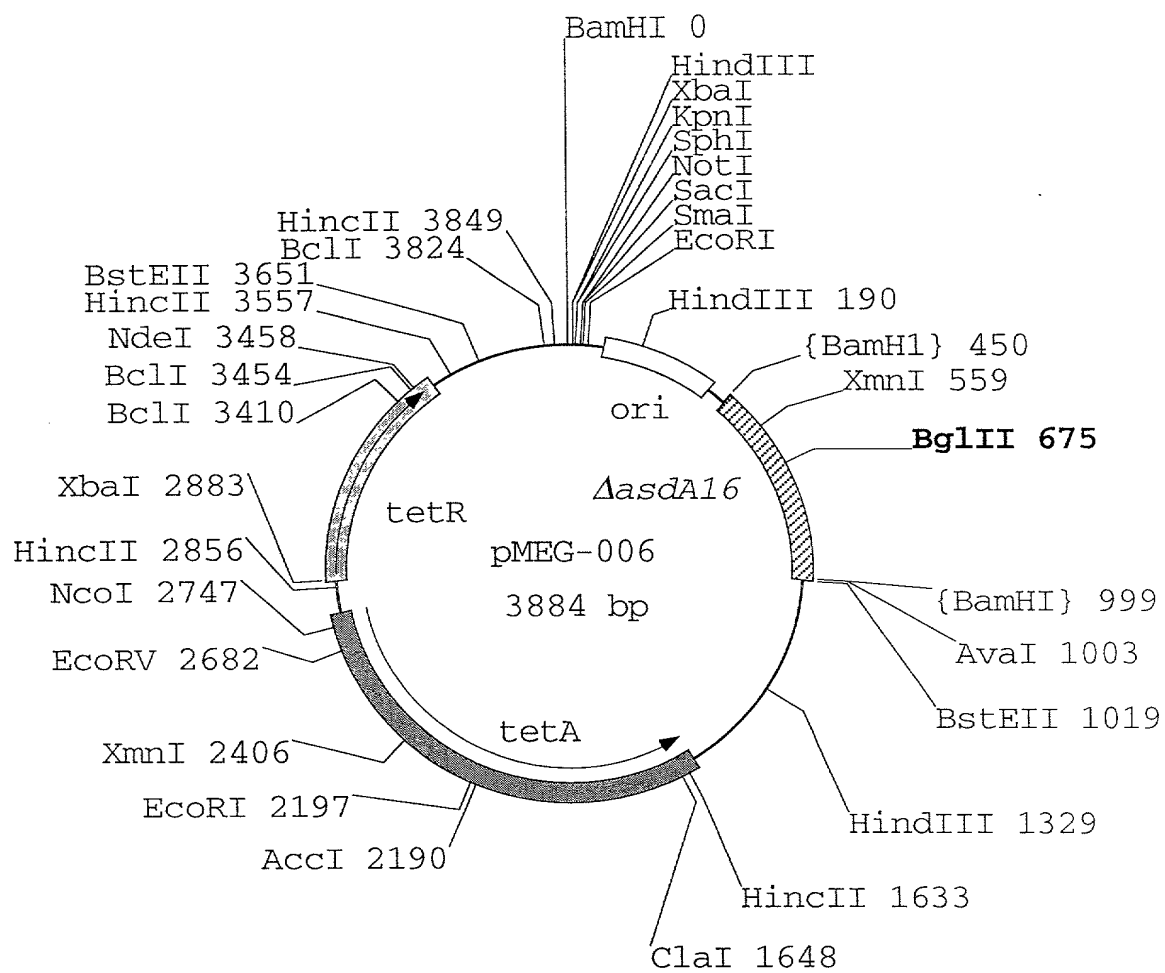
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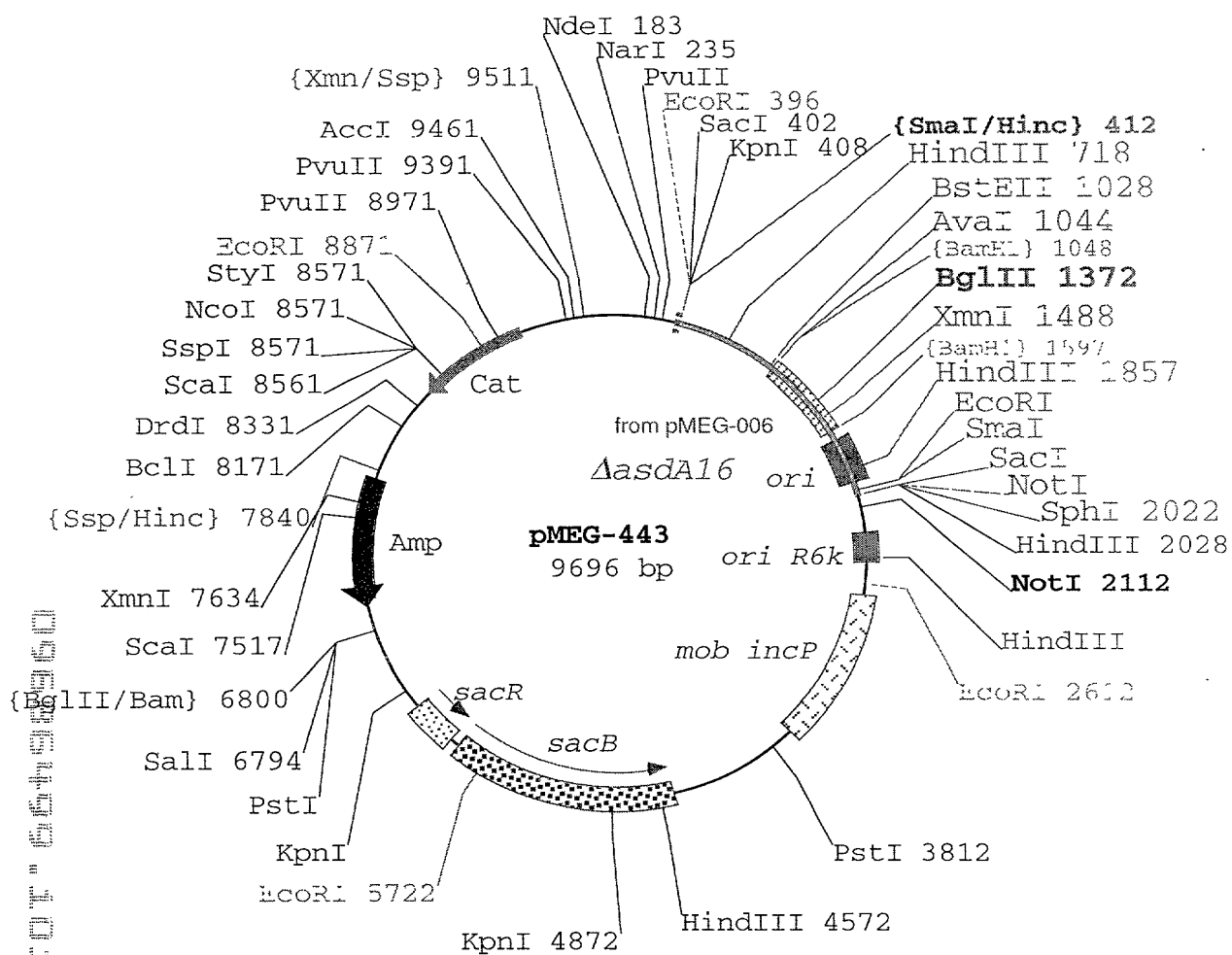
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LNTASVIPVDGLCVRVGALRCHSQAFTIKLKKEVSIPTVEELLA AHN PWAKVVPNDRDITMRELTAAV
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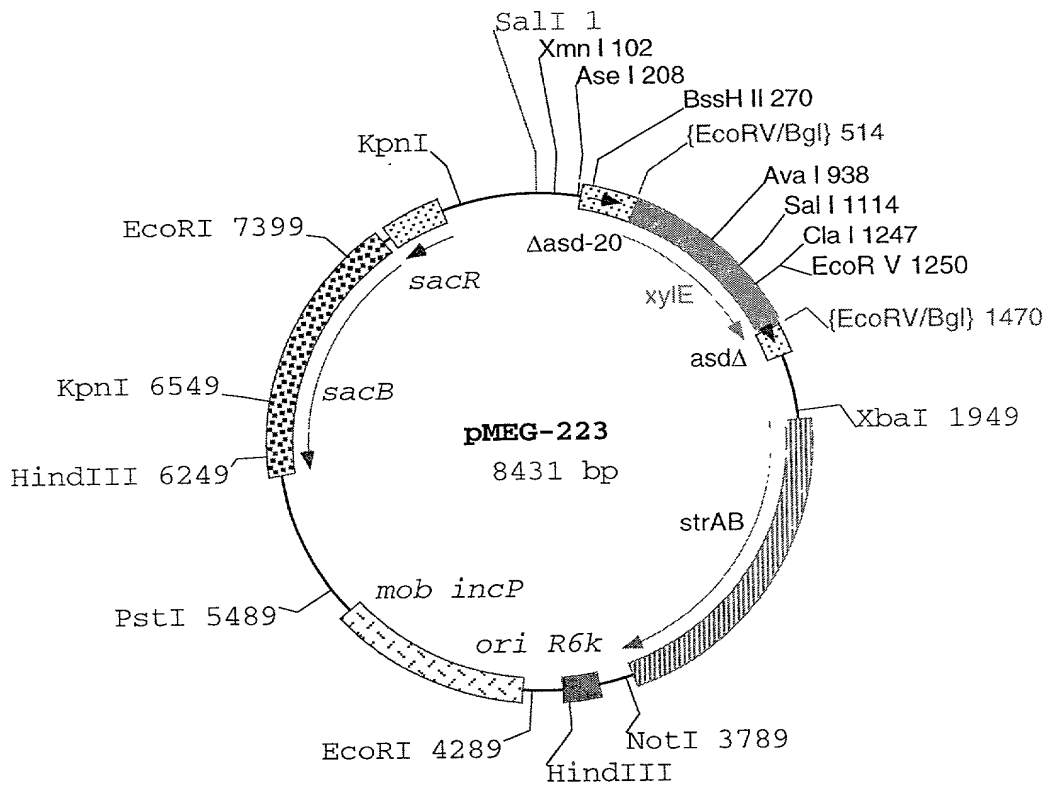


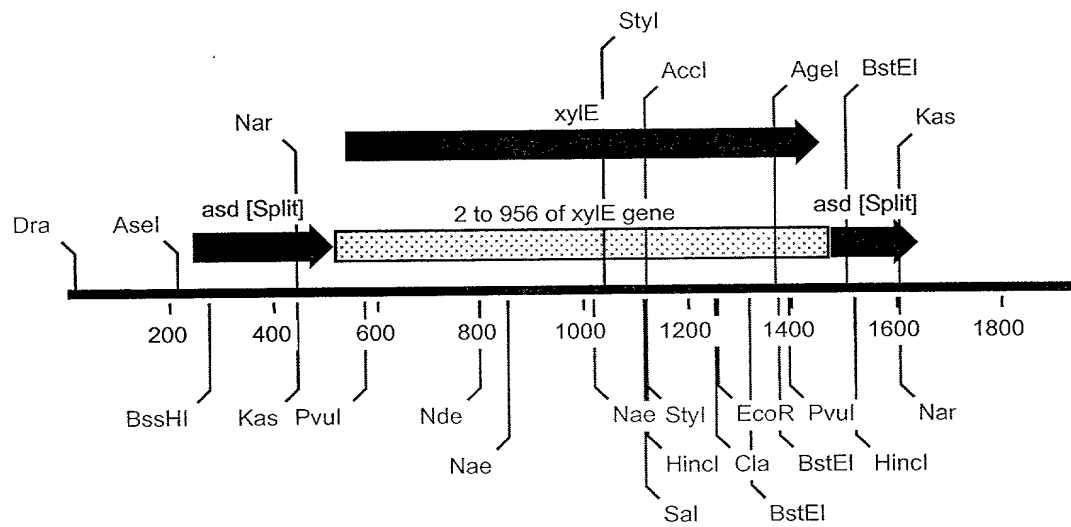
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{Be} = Be



096649.0400





22

AseI

BSSHII

380				390				400				410			420
GTA	GAG	GAG	CGC	GAT	TTC	GAC	GCT	ATT	CGC	CCT	GTT	TTC	TTT	TCT	
Val	Glu	Glu	Arg	Asp	Phe	Asp	Ala	Ile	Arg	Pro	Val	Phe	Phe	Ser	
a	a	a	a	a		ASD	[SPLIT]	a	a	a	a	a	a		

KasI

PvuII

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health status	Good	Fair		
Exercise frequency	Weekly	Monthly		
Stress level	Low	High		
Sleep quality	Good	Poor		
Dietary habits	Healthy	Unhealthy		
Alcohol consumption	None	Occasional		
Tobacco use	Non-smoker	Smoker		
Family size	2	3		
Work hours	40	50		
Commuting time	30	45		
Home ownership	Owner	Renter		
Neighborhood safety	Safe	Unsafe		
Access to green spaces	Yes	No		
Proximity to schools	Close	Far		
Public transportation	Good	Poor		
Crime rate	Low	High		
Weather conditions	Good	Poor		
Local economy	Strong	Weak		
Community involvement	High	Low		
Local government	Effective	Ineffective		
Local culture	Rich	Poor		
Local history	Interesting	Boring		
Local landmarks	Many	Few		
Local events	Frequent	Rare		
Local businesses	Diverse	Monotone		
Local infrastructure	Good	Poor		
Local services	Complete	Incomplete		
Local amenities	Many	Few		
Local attractions	Many	Few		
Local entertainment	Many	Few		
Local dining	Many	Few		
Local shopping	Many	Few		
Local healthcare	Good	Poor		
Local education	Good	Poor		
Local culture	Rich	Poor		
Local history	Interesting	Boring		
Local landmarks	Many	Few		
Local events	Frequent	Rare		
Local businesses	Diverse	Monotone		
Local infrastructure	Good	Poor		
Local services	Complete	Incomplete		
Local amenities	Many	Few		
Local attractions	Many	Few		
Local entertainment	Many	Few		
Local dining	Many	Few		
Local shopping	Many	Few		
Local healthcare	Good	Poor		
Local education	Good	Poor		

[illegible]

11

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112

116

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Abstract

Keywords:

1

134

Figure 1 consists of 12 sub-graphs (a-l) showing the time course of various physiological and behavioral parameters during the first 24 hours of a 28-day study. The parameters are: (a) Food intake (g), (b) Body weight (g), (c) Core temperature (°C), (d) Rectal temperature (°C), (e) Heart rate (b/min), (f) Respiratory rate (b/min), (g) Oxygen consumption (ml/min), (h) Energy expenditure (kcal/min), (i) Activity (min), (j) Sleep (min), (k) Locomotion (min), and (l) Rest (min). Each graph compares two groups: Control (open circles) and Experimental (filled circles). The x-axis for all graphs is 'Time (h)' from 0 to 24. The y-axis scales vary for each parameter. In general, the experimental group shows higher values for food intake, body weight, core temperature, rectal temperature, heart rate, respiratory rate, oxygen consumption, energy expenditure, activity, and locomotion, and lower values for sleep and rest compared to the control group.

1060 1070 1080 1090 1100
TAT CTG GCC GAA CAG GTG CTG GAC GAA AAT GGC ACG CGC GTC GCC
Tyr Leu Ala Glu Gln Val Leu Asp Glu Asn Gly Thr Arg Val Ala
____c____c____c____c____c____c____XYLE_____c____c____c____c____c____c

[illegible]

1420				1430				1440				1450
GAC	CGC	ATT	CTC	AAC	GAA	CGA	TTC	ATG	ACC	GTG	CTG	ACC
Asp	Arg	Ile	Leu	Asn	Glu	Arg	Phe	Met	Thr	Val	Leu	Thr
	C	C	C	C	C	XYLE		C	C	C	C	C

1460	1470	1480	1490	1500	
TGATGGTCCGGAGATC	ATC ACT ATG CGC GAA TTA ACC CCG GCG GCG GTG				
	Ile Thr Met Arg Glu Leu Thr Pro Ala Ala Val				
	b b b ASD [SPLIT] b b b b				

	1510			1520			1530			1540			1550	
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Thr	Gly	Thr	Leu	Thr	Thr	Pro	Val	Gly	Arg	Leu	Arg	Lys	Leu	Asn
b	b	b	b	b	ASD	[SPLIT]	b	b	b	b	b	b	b	b

		1560			1570			1580			1590				
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Met	Gly	Pro	Glu	Phe	Leu	Ser	Ala	Phe	Thr	Val	Gly	Asp	Gln	Leu	
	b	b	b	b	b	ASD	[SPLIT]	b	b	b	b	b	b	b	

KasI

1600		1610	1620	1630	1640
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Leu Trp Gly Ala Ala Glu Pro Leu Arg Arg Met Leu Arg Gln Leu					
b b b b b ASD [SPLIT] b b b b b b					

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Ala

1690 1700 1710 1720 1730 1740
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1750	1760	1770	1780	1790	1800
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1870	1880	1890	1900	1910	1920
TAAGCCTAACCTGAAGGTAGGACGACGCAGATAGGATGCACAGTGTGCTGCGCCGTT CAG					
1930	1940	1950	1960		
GTCAAAGAAGTGTCACTACCTGATGTTGAATTGGAAGATCC					

Variable	Mean	Standard deviation	Minimum	Maximum
Age	35.2	12.5	18	65
Gender	Male	10.5	0	20
Marital status	Married	15.2	0	20
Education	High school	12.5	0	20
Occupation	Unemployed	10.5	0	20
Income	Low	10.5	0	20
Health status	Good	15.2	0	20
Smoking status	Non-smoker	10.5	0	20
Alcohol consumption	Non-drinker	10.5	0	20
Exercise frequency	Low	10.5	0	20
Stress level	Low	10.5	0	20
Sleep quality	Good	15.2	0	20
Appetite	Good	15.2	0	20
Weight change	Stable	10.5	0	20
Blood pressure	Normal	15.2	0	20
Blood sugar	Normal	15.2	0	20
Cholesterol	Normal	15.2	0	20
Triglycerides	Normal	15.2	0	20
Hemoglobin A1c	Normal	15.2	0	20
Uric acid	Normal	15.2	0	20
Creatinine	Normal	15.2	0	20
Proteinuria	None	10.5	0	20
Diabetes	No	10.5	0	20
Hypertension	No	10.5	0	20
Heart disease	No	10.5	0	20
Stroke	No	10.5	0	20
Angina	No	10.5	0	20
Myocardial infarction	No	10.5	0	20
Heart failure	No	10.5	0	20
Arrhythmia	No	10.5	0	20
Valvular disease	No	10.5	0	20
Peripheral vascular disease	No	10.5	0	20
Chronic kidney disease	No	10.5	0	20
Liver disease	No	10.5	0	20
Autoimmune disease	No	10.5	0	20
Cancer	No	10.5	0	20
Depression	No	10.5	0	20
Anxiety	No	10.5	0	20
Substance use	No	10.5	0	20
Medication use	No	10.5	0	20
Compliance	High	15.2	0	20
Adherence	High	15.2	0	20
Healthcare utilization	Low	10.5	0	20
Health status	Good	15.2	0	20
Quality of life	Good	15.2	0	20
Satisfaction	High	15.2	0	20
Knowledge	High	15.2	0	20
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Beliefs	Positive	15.2	0	20
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Significance	Positive	15.2	0	20
Importance	Positive	15.2	0	20
Relevance	Positive	15.2	0	20
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Feasibility	Positive	15.2	0	20
Acceptability	Positive	15.2	0	20
Desirability	Positive	15.2	0	20
Viability	Positive	15.2	0	20
Profitability	Positive	15.2	0	20
Competitiveness	Positive	15.2	0	20
Marketability	Positive	15.2	0	20
Scalability	Positive	15.2	0	20
Sustainability	Positive	15.2	0	20
Resilience	Positive	15.2	0	20
Adaptability	Positive	15.2	0	20
Flexibility	Positive	15.2	0	20
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Quantity	Positive	15.2	0	20
Value	Positive	15.2	0	20
Cost	Positive	15.2	0	20
Time	Positive	15.2	0	20
Space	Positive	15.2	0	20
Energy	Positive	15.2	0	20
Information	Positive	15.2	0	

Nucleotide sequences of trc promoter/operator and MCS

MCS: *Nco*I *Eco*RI -----*Hind*III

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pYA3336, pYA3339, pYA3340, pYA3341, pYA3342

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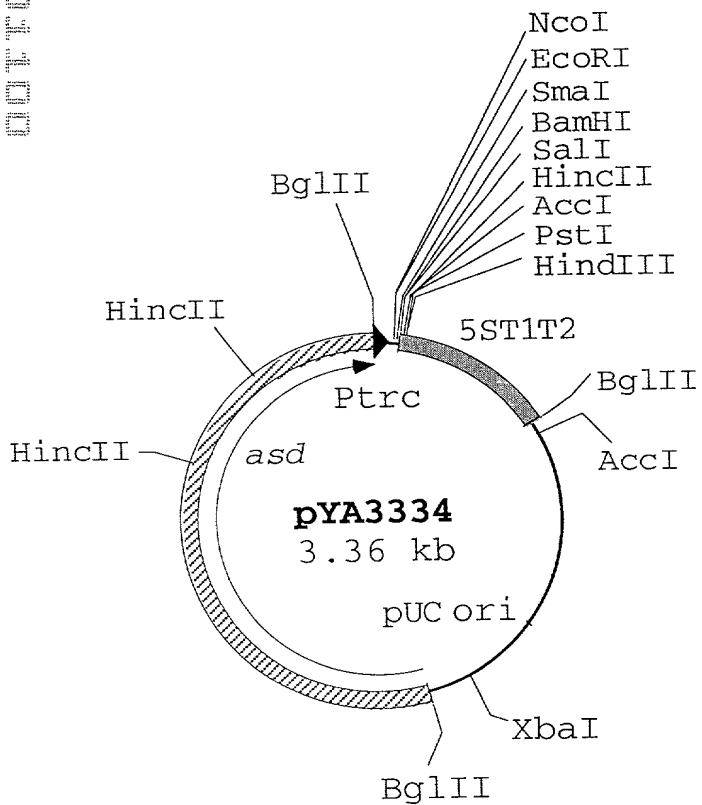
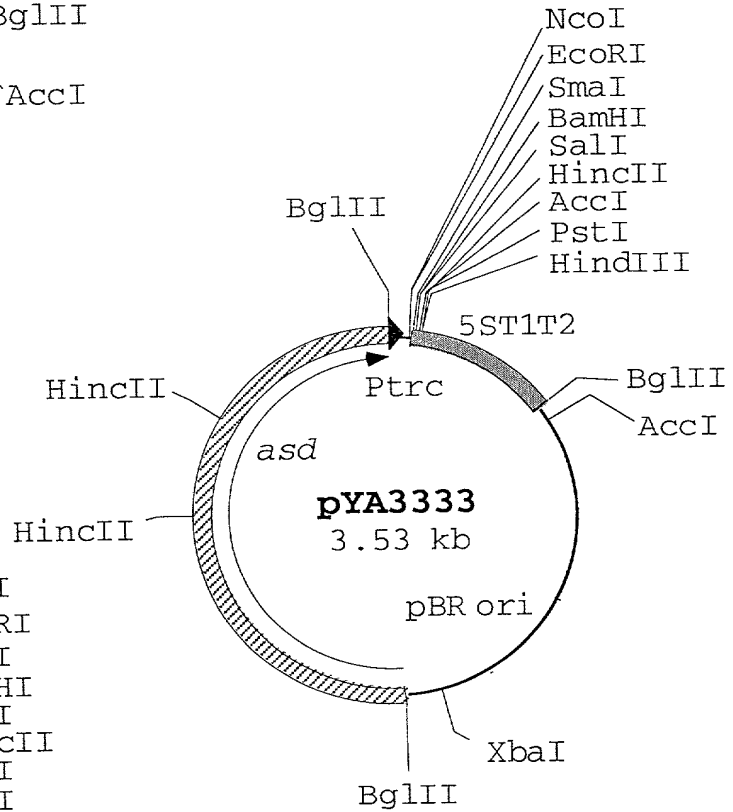
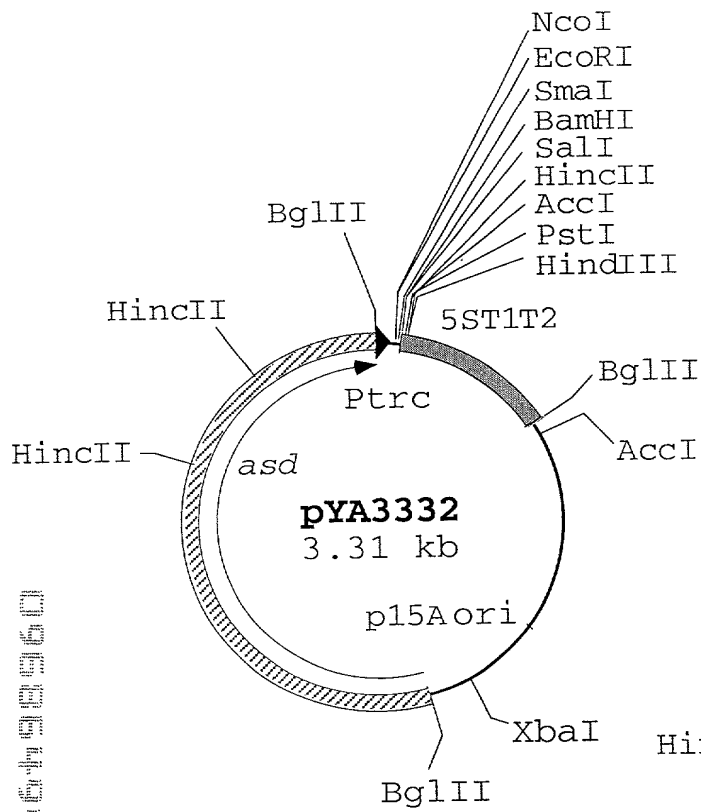
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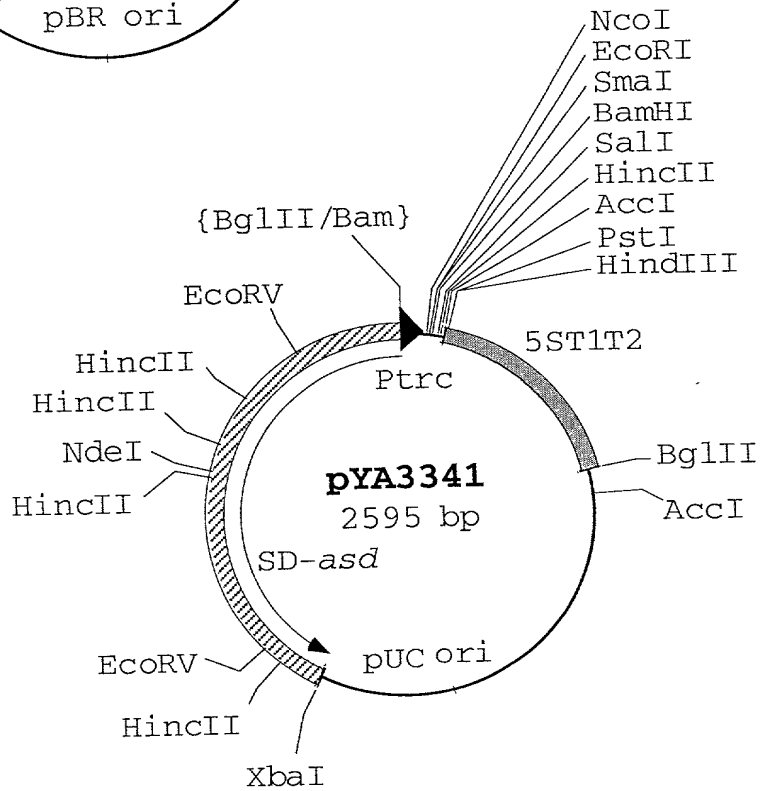
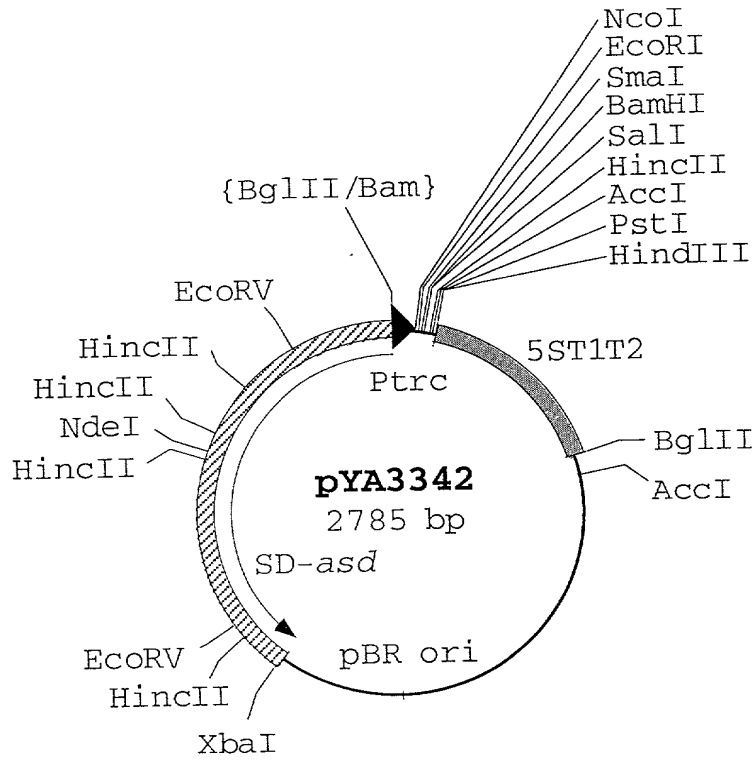
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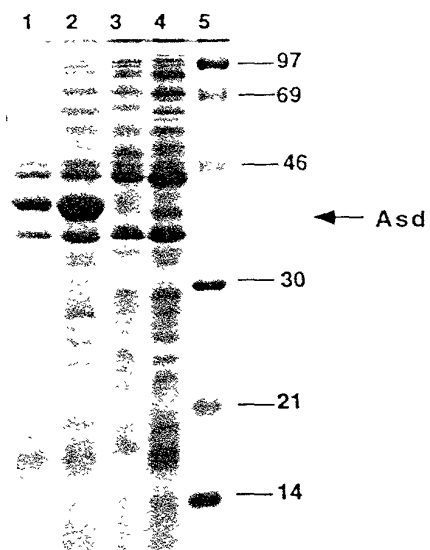
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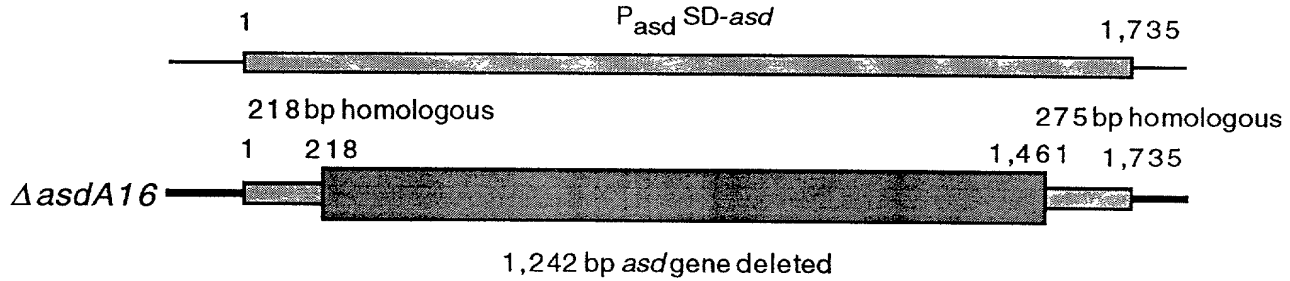


Level of Asd synthesized in recombinant
S. typhimurium strains with different Asd⁺ plasmids

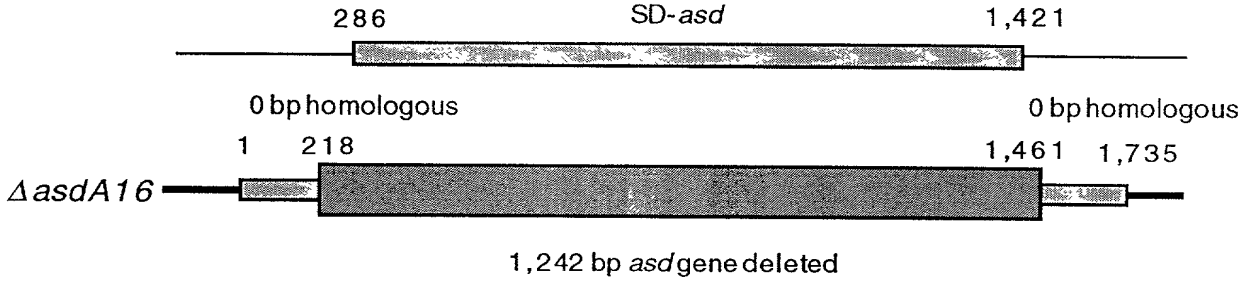


Cell lysates of *S. typhimurium* χ 4550 with pYA3333 (lane 1), pYA3334 (lane 2), pYA3342 (lane 3) and pYA3341 (lane 4). Lane 5 contains molecular weight markers. The arrow indicates Asd protein band.

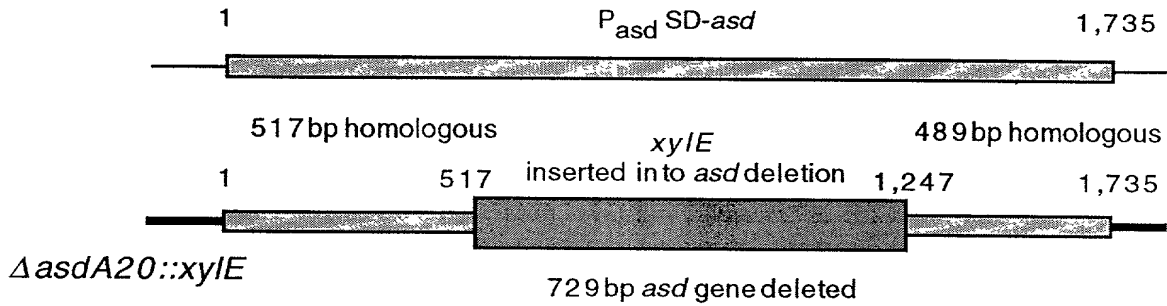
pYA3332, pYA3333 & pYA3334



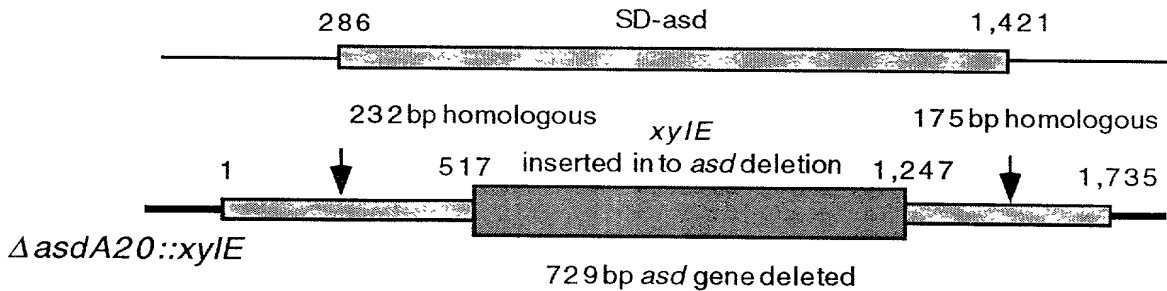
pYA3342 & pYA3341

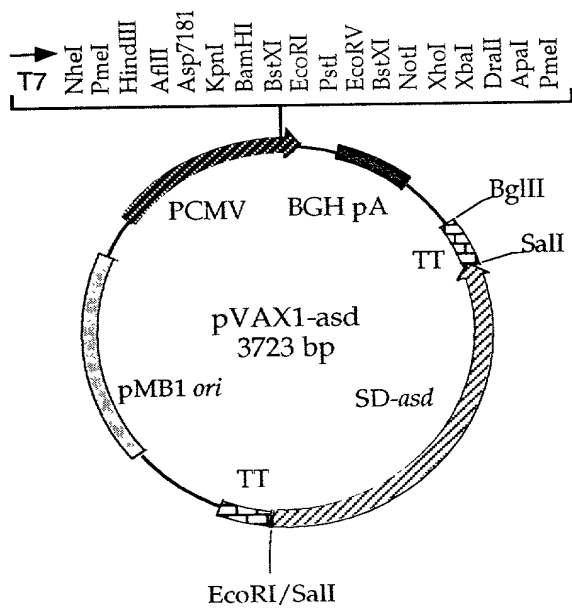


pYA3332, pYA3333 & pYA3334



pYA3342 & pYA3341





COMBINED DECLARATION AND POWER OF ATTORNEY(Original, Design, National Stage of PCT or CIP Application)

Inventors: Curtiss, Roy, III

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are stated below next to my name, I believe I am the original, first and sole inventor (if only one name is listed above) or an original, first and joint inventor along with those listed above (if plural names are listed above) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

FUNCTIONAL BALANCED-LETHAL HOST-VECTOR SYSTEMS

the specification of which: (Complete (a), (b) or (c) for type of application)

REGULAR OR DESIGN APPLICATION

- (a) x is attached hereto.
- (b) was filed on as Application Serial No. and was amended on (if applicable).

PCT FILED APPLICATION ENTERING NATIONAL STAGE

- (c) was described and claimed in International Application No. filed on and as amended on (if any).

ACKNOWLEDGEMENT OF REVIEW OF PAPERS AND DUTY OF CANDOR

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations §1.56.

 In compliance with this duty there is attached an information disclosure statement.
37 CFR 1.97.

PRIORITY CLAIM

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

[Complete (d) or (e)]

- (d) _____ no such applications have been filed.
- (e) _____ such applications have been filed as follows.

EARLIEST FOREIGN APPLICATION(S), IF ANY FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO SAID APPLICATION

Country	Application No.	Date of filing (day, month, year)	Date of issue (day, month, year)	Priority (day, month, year)	Claimed
_____	_____	_____	_____	_____	____ YES NO ____
_____	_____	_____	_____	_____	____ YES NO ____
_____	_____	_____	_____	_____	_____

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO SAID APPLICATION

CLAIM FOR BENEFIT OF PRIOR U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under Title 35, United States code, § 119(e) of any United States provisional application(s) listed below:

_____	_____
(Provisional Application Number)	(Filing Date)
_____	_____
(Provisional Application Number)	(Filing Date)
_____	_____
(Provisional Application Number)	(Filing Date)

CONTINUATION-IN-PART

(Complete this part only if this is a continuation-in-part application)

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

(Application Serial No.)	(Filing Date)	(Status)	(Patent, pending, abandoned)
--------------------------	---------------	----------	------------------------------

(Application Serial No.)	(Filing Date)	(Status)	(Patent, pending, abandoned)
--------------------------	---------------	----------	------------------------------

POWER OF ATTORNEY

As a named inventor, I hereby appoint the following attorney and/or agent to prosecute this application and transact all business in the U.S. Patent and Trademark Office connected therewith, before all competent international authorities in connection with any international application, and before all foreign patent offices in connection with the national phase of any international application or any foreign application, and to appoint any associate attorneys in connection with any application, either domestic, international or foreign national.

John M. Howell (25,261); Richard E. Haferkamp (29,072); Kenneth Solomon (31,427); Joseph M. Rolnicki (32,653); Alan H. Norman (32,285); Anthony G. Simon (40,813); Thomas A. Polcyn (41,256); David B. Jenkins (46,805); Jeffrey H. Urian (46,232); Clyde L. Smith (46,292); Elie H. Gendloff (44,704); Daniel S. Kasten (45,363)

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor Roy Curtiss, III

Inventor's signature

Date

10-11-00

Country of Citizenship United States

Residence 6065 Lindell Boulevard, St. Louis, Missouri 63112

Post Office Address 6065 Lindell Boulevard, St. Louis, Missouri 63112

SEQUENCE LISTING

<110> CURTISS III, Roy

<120> FUNCTIONAL BALANCED-LETHAL HOST-VECTOR SYSTEMS

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